

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 23, 2006, 22:28:26 ; Search time 7449 Seconds
(without alignments)

10810.020 Million cell updates/sec

Title: US-10-678-023a-1

Perfect score: 1439.2

Sequence: 1 tggagagttgatcctggct.....agaagtggtaggtaaccg 1440

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_est7:*
- 7: gb_est8:*
- 8: gb_est9:*
- 9: gb_est10:*
- 10: gb_est11:*
- 11: gb_est12:*
- 12: gb_est13:*
- 13: gb_est14:*
- 14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	799.8	55.6	6499	11	BH771024
2	716.8	49.8	1954	8	CX109203
C 3	655.4	45.5	793	13	DU370470
4	633.2	44.0	941	5	CK296497
5	615.8	42.8	1084	11	BZ439740
C 6	613.8	42.6	1053	11	BZ447500
C 7	608	42.2	1010	11	BZ431523
8	602.8	41.9	1033	14	DU743187
C 9	602.4	41.9	1016	11	BZ426201
10	599.4	41.6	889	5	CK280527
C 11	599.4	41.6	1143	11	BH814966
12	599	41.6	1079	11	BH705272
C 13	595.8	41.4	976	14	DU733613
14	592.8	41.2	884	5	CK280528
15	592.8	41.2	917	14	DU476609
C 16	591	41.1	1031	11	BH656222
C 17	585.4	40.7	1044	11	BZ463550
C 18	584.4	40.7	1051	11	BZ494182
C 19	585.8	40.6	899	12	BZ685785

20	581.2	40.4	1077	11	BZ450751
21	576	40.0	861	14	DU486180
22	573	39.8	746	11	AQ957362
23	572.8	39.8	787	8	CO159272
24	568	39.5	845	14	DU477685
25	566.8	39.4	863	14	DU487250
26	564.6	39.2	840	14	DU478845
27	563	39.1	974	11	BZ440868
28	560.8	39.0	810	14	DU477669
29	560.2	38.9	854	14	DU477664
C 30	558.8	38.8	716	11	AQ957363
C 31	558.4	38.8	1054	11	BH647750
C 32	558	38.8	894	14	DU487242
33	554.6	38.5	830	14	DU476605
C 34	552.8	38.4	890	14	DU476594
C 35	552.6	38.4	756	9	DN469396
C 36	552.6	38.4	851	5	CK290947
C 37	550.6	38.3	1106	11	BZ469058
C 38	549.4	38.2	860	8	CN757363
C 39	547.2	38.0	1069	11	BZ474941
C 40	545.8	37.9	924	13	DU101928
C 41	543.4	37.8	951	11	BH651765
C 42	540.2	37.5	957	14	DU744805
C 43	540	37.4	861	14	DU486177
C 44	537.8	37.4	861	14	DU486177
C 45	537.4	37.3	977	11	BZ459292

ALIGNMENTS

RESULT 1
LOCUS BH771024 6499 bp DNA linear GSS 01-MAY-2002
DEFINITION LLMGtag746 MG1363 Random Sequence Tag Library Lactococcus lactis subsp. cremoris genomic, genomic survey sequence.
ACCESSION BH771024
VERSION BH771024.1 GI:20373981
KEYWORDS GSS.
SOURCE Lactococcus lactis subsp. cremoris
ORGANISM Lactococcus lactis subsp. cremoris
REFERENCE 1 (bases 1 to 6499)
AUTHORS Bolotin.A., Ehrlich.S.D. and Sorokin.A.
TITLE Studies of genomes of dairy bacteria Lactococcus lactis
JOURNAL Sci. Aliments (2002) In press
COMMENT Contact: Sorokin A
Genetique Microbienne
INRA
CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
best homologue in strain ILI403 is ywGA (78%)
Class: shotgun
High quality sequence start: 30
High quality sequence stop: 6471.
Location/Qualifiers
1. .6499
/organism="Lactococcus lactis subsp. cremoris"
/mol_type="genomic DNA"
/strain="MG1363"
/sub_species="cremoris"
/db_xref="taxon:1359"
/clone_lib="MG1363 Random Sequence Tag Library"
/note="Vector: pSGM2; Site 1: SmaI; Library of chromosomal fragments of L.lactis strain MG1363 was prepared by partial AluI digestion or by sonication."

ORIGIN

Query Match 55.6%; Score 799.8; DB 11; Length 6499;
Best Local Similarity 76.0%; Pred. No. 1.7e-234;

Matches 1106; Conservative 1; Mismatches 329; Indels 19; Gaps 9;	
Qy	1 TGGAGAGTTTGAATCCTGGCTCAGATTGAAACGCTGGCGGCATGCTTTTACATGCAATGTCG 60
Db	
529	TTGAGAGTTTGAATCCTGGCTCAGGACGAAACGCTGGCGGCGTGCCTAATACATGCAAGTTG 588
Qy	61 AAGC--GTAACAGAGTCTTGCACCC--GCTACACAGTGGCGAAGCGGTGAGTAAATCGT- 115
Db	
589	AGCGATGAAGATTGGTGTCTTGACAAATTTGAAGAGCAGCAACGCGGTGAGTAAACGGGTG 648
Qy	116 CGGAATGTACCGTGAATGGGGGATAGCTCGCGGAAAGCCGGAATTAATACCGCATACGCC 175
Db	
649	GGGAATCTGCCCTTTGAGCGGGGACAACATTTGGAACGAATGCTAATACCGCATATAA 708
Qy	176 CT-----GAGGGGAAAGCGGGGATCGAAGACCTCGGTTATACGAGCAGCCGACG 228
Db	
709	CTTTAAACATAAAGTTTAAAGTTTGAAGATGCAATTTGCATCACTCAAAGATGATCCCGCG 768
Qy	229 TCTGATTAGCTAGTTGGTGAAGTAAGAGCTCACCAAGCGACGATCAGTAGCGGTTCTGA 288
Db	
769	TTGTAATTAGCTAGTTGGTGAAGTAAGAGCTCACCAAGCGGATGATACATACCGACCTGA 828
Qy	289 GAGGATGATCCGCCACACTGGGACTGAGACACGGCCAGACTCTCTACGGGAGGCGAGT 348
Db	
829	GAGGTTGATCGGCCACACTTTGGACTGAGACACGGCCCAAACTCTCTACGGGAGGCGAGT 888
Qy	349 GGGGAATTTTGACAAATGGGGGCAACCTGATCAGCCATGCCCGCTGCTGAAGAAGGC 408
Db	
889	AGGGAATCTTCGGCAATGGACGAAAGTCTGACCGAGCAACCGCCGCTGAGTGAAGAAGGT 948
Qy	409 CTTGGGTTGTAAAGGACTTTTGTGAGGGGAAATCCCGTGTGTTAATACCCGCGGGG 468
Db	
949	TTTCGGATCGTAATAACTCTGTGTTAGAGAAAGACGTTGGTAGAGTGGAAGCTCATCA 1008
Qy	469 A-TGACAGTACCBGAAGAATAAGCACCGCTAACTAGCTGCACAGCCGCGGTAAATACG 527
Db	
1009	AGTGACGTAATACTACCCAGAAAGGACGGCTAACTAGCTGCACAGCCGCGGTAAATACG 1068
Qy	528 TAGGTTGACAGCGTTAATCGGAATTAATCGGCGTTAAGCGTGAAGCGCGGTTTTGCAAG 587
Db	
1069	TAGTCCCGAGCGTTGTCCGAATTTATTGGCGGTAAAGCGAGCGCAGGTGTTTATTAAAG 1128
Qy	588 TCTGATGTGAAGCCCGGGCTCAACCTGGGAAACGGCAATGGAGACTGCAAGACTAGAGT 647
Db	
1129	TCTGTTGTAAGAAGCAGTGGCTCAACCATTTGTA-TGCATTGGAACCTGGTAGACTTGAGT 1187
Qy	648 CGCTCAGAGGGGGTAGAATTTCCCGTGTAGCAGTGAATCCGTAGAGATCGGAGGAAT 707
Db	
1188	GCAGGAGAGGAGAGTGGAAATTTCCATGTGTAGCGGTGAAATCGGTAGATATATCGAGGAAC 1247
Qy	708 ACCGATGCGGAAGCAGCGCCCTGGGATGACACTGACGCTCATGCAGAAAGCGTGGGA 767
Db	
1248	ACCGGTGCGAAAGCGGCTCTCTGCGCTGTAACTGACACTGAGGCTGAAAGCGTGGGA 1307
Qy	768 GCAAAACAGATTAGATACCTGTGAGTCCAGCCCTAAACGATGTCATTAAGCTGTTGGG 827
Db	
1308	GCAAAACAGATTAGATACCTGTGAGTCCAGCCGTAAACGATGAGTGTAGATGTAGGG 1367
Qy	828 -GGTTTGAATCCTTGGTAGCGTAGCTAACCGGTGAAATTTGACCGCTGGGAGTACGGCC 886
Db	
1368	AGCTATAAGTTCTCTGTATCGCAGCTAACGCAATAAGCACTCCGCTGGGAGTACGACC 1427
Qy	887 GCAGGTTAAACTCAAGGAATTGACGGGACCCGCACAGCGGTGGATGATGCGATT 946
Db	
1428	GCAAGGTTGAAACTCAAGGAATTGACGGGCGCCGCACAGCGGTGGAGCATGTGGTTT 1487
Qy	947 AATTCGATGCAACGCGGAAACCTTACCTGCTCTTGACATGTAGC-GAACTTGTGTAGAGA 1005
Db	
1488	AATTCGAGCAACGCGGAAGACCTTACAGGCTCTTGACATACTCGTGTATTCTCTAGAGA 1547
Qy	1006 TATCTTGTGCGCCGAAAGGGAGCCGTAAACAGGTTGCTGCATGGCTGTCAGTCTGCTG 1065
Db	
1548	TA---GGAAGTTTCTTTCGGGACACGGGATACAGGTGCTGATGTTGTCGTGAGTCTGCTG 1604

Qy	1066 TCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCTTCTCATTTAGTTGCCATCAT 1125
Db	
1605	TCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCTTATTTAGTTGCCATCAT 1664
Qy	1126 TTAGTTGGGCACCTCTAATGAGACTGCGGGTGACAAACCGGAGGAAGTGGGGATGACGTC 1185
Db	
1665	TAAGTTGGGCACCTAACGAGACTGCGGGTGATAAAACCGGAGGAAGTGGGGATGACGTC 1724
Qy	1186 AAGTCTCATGCGCCCTTATGAGCAGGGCTTACACGCTCATACAATGGTGGGTACAGAGG 1245
Db	
1725	AAATCATCATGCCCTTATGACCTGGGCTACACACGCTGCTACAATGGATGGTACAACGAG 1784
Qy	1246 TCGCTAAGCGCGAGGTGGTCCAATCTCATAAACCGATCGTAGTCCGGATCGCACTCT 1305
Db	
1785	TCGCGAGACAGTATGATTTAGCTTAATCTCTTAAACCATCTCAGTTCGATTGTAGGCT 1844
Qy	1306 GCAACTCGAGTGGCGTGAAGTCGGAATCGCTAGTAATTCGAGATCAGCATGCTCGCGTGAA 1365
Db	
1845	GCAACTCGCCTACATGAAGTCGGAATCGCTAGTAATTCGCGGATCAGCACGCCGCGTGAA 1904
Qy	1366 TAGCTTCCCGGGCTTTGTACACACCGCCGCTACACCATGGGAGTGAGTTTACCCAGAA 1425
Db	
1905	TACGTTCCCGGGCTTTGTACACACCGCCGCTACACCAAGGGAGTTGGGGAGTACCCGAAG 1964
Qy	1426 TGGTAGGCTTAACCG 1440
Db	
1965	TAGTTGCTTAACCG 1979

RESULT 2
CX109203
LOCUS
DEFINITION
RECM0593 A normalized whole-life-cycle cDNA library of rice Oryza sativa (indica cultivar-group) cDNA clone EI051022, EI053008, EI008B17, BI076L19, BI154A06, BI133B10, EI11 5', mRNA sequence.
CX109203
VERSION
CX109203.1 GI:66922355
KEYWORDS
EST.
SOURCE
Oryza sativa (indica cultivar-group)
ORGANISM
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 1954)
AUTHORS
Zhang,J., Feng,Q., Jin,C., Qiu,D., Zhang,L., Xie,K., Yuan,D., Han,B., Zhang,Q. and Wang,S.
TITLE
Features of the expressed sequences revealed by a large-scale analysis of ESTs from a normalized cDNA library of the elite indica rice cultivar Minghui 63
JOURNAL
Plant J. 42 (5), 772-780 (2005)
PUBMED
15918889
COMMENT
Contact: Wang S
National Key Laboratory of Crop Genetic Improvement
Hauzhong Agricultural University
Wuhan 430070, China
Tel: 86-27-87282044
Fax: 86-27-87287092
Email: shiyingwang@hotmail.com
Seq primer: T7.
FEATURES
Seq primer: T7.
Location/Qualifiers
1..1954
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/strain="indica"
/cultivar="Minghui 63"
/db_xref="taxon:39946"
/c1one="EI051022, EI053J08, EI008B17, BI076L19, BI154A06, BI133B10, EI11"
/tissue_type="whole plant"
/dev_stage="whole-life-cycle"
/lab_host="E. coli DH10B"
/clone_lib="A normalized whole-life-cycle cDNA library of


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/organism="Ovis aries"
/mol_type="genomic DNA"
/strain="Texel breed"
/db_xref="taxon:9940"
/clone="CH243-111G6"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-243"
/notes="vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
The CHORI-243 sheep (M) (Ovis aries) BAC library produced
by Pieter de Jong's lab at CHORI
http://bacpac.chori.org/library.php?id=162"

ORIGIN
Query Match 45.5%; Score 655.4; DB 13; Length 793;
Best Local Similarity 90.7%; Pred. No. 3.2e-190;
Matches 721; Conservative 0; Mismatches 71; Indels 3; Gaps 2;

Qy 565 GCGTGGCCAGCGGTTTGCAGTCTGATGTGAAGCCCGGCTCAACCTGGGACGGC 624
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 793 GCGAGCCGACGCGTTTATTAAAGCAAGATGTGATCCCGAGCTTAACCTTGGGAATGC 734
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 625 ATTGAGACTGCAAGACTAGAGTCGTCAGAGGGGGGTAGATATCCCGTGTAGCAGTGA 684
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 733 GTTTTGAACCTGTAAGCTAGATATGTGAGGGGGGTAGATATCCAGTGTAGCAGTGA 674
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 685 AATCGGTAGATCGGAGGAATACCGATGCGAAGGACGCCCTCGGATGACACTGAC 744
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 673 AATCGGTAGATGTGAGGAATACCGATGCGAAGGACGCCCTCGGATGACTGAC 614
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 745 GCTATGACGAAGCGTGGGAGCAACAGGATTAGATACCTGCTAGTCCAGCCCTA 804
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 613 GTTCATGCTCGAAAGCGTGGGTAGCAACAGGATTAGATACCTGCTAGTCCAGCCCTA 554
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 805 AACGATGTCATTAAGCTGTTGGG-GGTTTGAATCCTTTGGTAGCGTAGCTAACGCGTGA 863
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 553 AACGATGTCATTAAGCTGTTGGGCAACATGATTCCTTAGTAGCTAGCTAACGCGTGA 494
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 864 TTGACCGCTGGGAGTACGCGCCGACAGTGTAAACCTCAAGGAATTGACGGGACCCGC 923
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 493 TTGACCGCTGGGAGTACGCTCGCAAGATATTAACCTCAAGGAATTGACGGGACCCGC 434
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 924 ACAGCGGTGATCATGTGGATTAATTCGATGCAACGCGAAACCTTACCTGCTTTGA 983
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 433 ACAAGCGGTGATGATGTGGATTAATTCGATGCAACGCGAAACCTTACCTGCTTTGA 374
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 984 CATGTACGGAACTTTGGTAGAGATATCTTTGGTSCCCGAAAGGGAGCCGTAACACAGGTGCT 1043
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 373 CATGTACGGAACTTCCAGAGACGGAAGAGTGCCTTC--GGAGCCGTTAACACAGGTGCT 316
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1044 GCATGGCTGCTCAGCTCGTGTGCGTAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC 1103
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 315 GCATGGCTGCTCAGCTCGTGTGCGTAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC 256
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1104 CCTGTGCTATTAGTGGCAATATTAGTTGGGCACCTCTAATCAGACTGCGCGTGACAAACC 1163
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 255 CCTGTGCTATTAGTGGCCACCATTCACTTGGGCACCTTTAATGAGACTGCGCGTGACAAACC 196
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1164 GGAGGAAGTGGGATGACGTCAGAGTCTCTATGGCCCTTATGAGCAGGGCTTTCACAGTC 1223
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 195 GGAGGAAGTGGGATGACGTCAGAGTCTCTATGGCCCTTATGACAGGGCTTTCACAGTC 136
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1224 ATACATGGTGGGTACAGAGGCTGCTAAGCCGGGAGTGTGCGCAATCTCATTAACCCG 1283
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 135 ATACATGGTGGGTACAGAGGCTGACCAAGCCGGGAGTGGAGCCAACTTCAGAAAAACC 76
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1284 ATCTGTGTCGGATCGCACTCTGCAACTCGAGTGGTGAAGTCGGAATCGGTAGTAATCG 1343
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 75 ATCTGTGTCGGATGTCACCTCTGCAACTCGAGTGCATGCAAGTCCGATCGGTATGATCG 16
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1344 CAGATCAGCATGCTG 1358
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 15 CAGGTACGACTACTG 1
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 4
CK296497 941 bp mRNA linear EST 02-AUG-2004
LOCUS EST759211 Nicotiana benthamiana mixed tissue cDNA library,
DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NBMD226 5',
end, mRNA sequence.
CK296497
CK296497.1 GI:39881943
EST.
Nicotiana benthamiana
Nicotiana benthamiana
Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
Staskawicz,B., Jin,H. and Baker,B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
FEATURES
Location/Qualifiers
1..941
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NBMD226"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/notes="Vector: pCMVSPORT6.1; Site_1: EcoRI; Site_2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."
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ORIGIN
Query Match 44.0%; Score 633.2; DB 5; Length 941;
Best Local Similarity 81.5%; Pred. No. 2.4e-183;
Matches 768; Conservative 1; Mismatches 170; Indels 3; Gaps 3;

Qy 7 GTTTGATCCTGGCTCAGATTGAACGCTGGCGCATGCTTTACACATGCAAGTCGAACCGT 66
Db 1 GTTTGATCATGGCTCAGATTGAACGCTGGCGCAGGCTTAACATGCAAGTCGAGCGGC 60
Qy 67 AACAA-GGGTGCTTGCACC-GCTGACGAGTGGCGAACGGGTGAGTAATGCGTCGGAATGTA 124
Db 61 AGCAGCGGTACTTGTACTCTGTTGGCAGCGCGGAGTGAATATGCTCTAGGAATCTG 120
Qy 125 CCGTGTAAATGGGGATAGCTCGCGGAAAGCCGGATTATATCCGATACGCCCTGAGGGG 184
Db 121 CCTGTGTAGTGGGGATAACGCTCGGAAACCGACGCTAATACCGCATACGCTCTACGGGAG 180
Qy 185 AAACCGGGGATCGAAAGACCTCGCGTTTATACGAGCAGCCGACCTCTGATTAGCTAGTTG 244
Db 181 AAAGCAGGGGACCTTCGGGGCTTCGGCTTATCAGATGAGCCCTAGGTCCGATTAGCTAGTTG 240
Qy 245 GTGAGGTAAGAGCTCACCAGGCGACGATCATGTAGCGGGTCTGAGAGGATGATCGGCCAC 304
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|||||
241 GTGAGTAATGGCTCACCAGGCGACGATCGTAACCTGGTCTGAGAGGATGATCAGTCAC 300
QY |||||
305 ACTGGGACTGAGACACGGCCAGACTCTCTAGGGAGGCGACAGTGGGAATTTTGGACAA 364
Db |||||
301 ACTGGAATCTGAGACACGGTCCAGACTCTCTAGGGAGGCGACAGTGGGGAATATTTGACAA 360
QY |||||
365 TGGGGCAACCTCTGATCCAGCCATCGCCGCTGTCTGAAGAAGCGCTTTCGGGTTGTAAAGG 424
Db |||||
361 TGGGCGAAGCCTGATCCAGCCATCGCCGCTGTCTGAAGAAGCTTTCGGATTGTAAAGC 420
QY |||||
425 ACTTTTGTGAGGAGGAAATCCCGCTGGTTAAATACCCGGCGGGGATGACAGTACCBGAAG 484
Db |||||
421 ACTTTTAAGTTTGGGAGGAAGCGCAGTTACCTAATACGTGATGTTGTTTGACCGCTTACCGACAG 480
QY |||||
485 AATAAGCACCGGCTAATCTAGTCCAGCAGCGCGGTAATACGTAGGTCGCAAGCGTTAA 544
Db |||||
481 AATAAGCACCGGCTAATCTAGTCCAGCAGCGCGGTAATACGTAGGTCGCAAGCGTTAA 540
QY |||||
545 TCGGAAATTAATGCGCGTAAAGCGTGCAGCGCGGTTTTCGCAAGTCTGATGTGAAAGCCCC 604
Db |||||
541 TCGGAAATTAATGCGCGTAAAGCGGCTAGTGGTTTGTAAAGTTGAAATCCCTCC 600
QY |||||
605 GGGCTCAACCTGGGAACGGCAATTTGGAGACTGCAAGACTAGAGTGCCTCAGAGGGGGTAG 664
Db |||||
601 GGGCTCAACCTGGGAACCTGCAATCCAAATCTGGCAAGCTAGAGTATGCTAGAGCGTGTGG 660
QY |||||
665 AATTCGCGGTAGCAGTGAATGCGTAGAGATCGGAGGAATACCGATGCGCAAGCGCAG 724
Db |||||
661 AATTTCTGTGTAGCGGTGAATGCGTAGATATAGGAAGGAACACCAAGTGGCGAAGCGCA 720
QY |||||
725 CCCCTGGGATGACACTGACGCTCATGCACGAAAGCGTGGGAGCAAAACAGGATTAGATA 784
Db |||||
721 CCACCTGGAATGACTGACACTGAGGTGCGAAAGCGTGGGAGCAAAACAGGATTAGATA 780
QY |||||
785 CCCTGTAGTCCACGCGCTTAACGATGTCAATTAAGTGTGTTGGGGTTTGAATCCTTGGTA 844
Db |||||
781 CCCTGTAGTCCACGCGCTTAACGATGTCAATTAAGTGTGTTGGGGTTTGAATCCTTGGTA 840
QY |||||
845 GCGTGTAGTCCACGCGTGAATTAAGCGCTGCGGAGTACGCGCAAGGTTTAAACTCAAA 904
Db |||||
841 G-GGAGTAAACGATTAAGTTGACCGCTTGGGAGTACGCGCCCGCAGGTTTAAACTCAAA 899
QY |||||
905 GGAATTGACGGGACCGCACAGCGGTGATGTGGATT 946
Db |||||
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RESULT 5

BZ439740
LOCUS BONDUS4TF BO_1.6_2_KB_tot Brassica oleracea genomic clone BONDUS4,
DEFINITION genomic survey sequence.

ACCESSION BZ439740

VERSION BZ439740.1

KEYWORDS GI:26695676

SOURCE GSS.

ORGANISM Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 1084)

Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,

Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D.

Whole genome shotgun sequencing of Brassica oleracea and its

application to gene discovery and annotation in Arabidopsis

Genome Res. 15 (4), 487-495 (2005)

15805490

Other GSSs: BONDUS4TR

Contact: Chris Town

TIGR Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TP
Class: sheared ends.
Location/Qualifiers
source 1..1084
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
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/notes="Vector: pHOs1; Site 1: BstXI; 1.6-2 kb sheared
total DNA inserted into pHOs1 using BstXI linkers"

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Best Local Similarity 75.8%; Pred. No. 5.8e-178;
Matches 824; Conservative 1; Mismatches 234; Indels 28; Gaps 4;
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QY 382 CAGCCATCGCGGTGTCTGAAGAAGCCCTTCGGGTTGTAAAGACTTTTGTTCAGGGAGGA 441
Db 126 GAGCAATCGCGGTGGAGGTAGAAAGCCCTACGGGTCTGAACTCTCTTTCCAGAGAGA 185
QY 442 AATCCCGCTGTTAATACCCGGCGGGATGACAGTACCBGNAAGATAAGCACCGGCTAAC 501
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QY 502 TAGTGCCAGCAGCCCGGTAAATACGTAGGTTGCAAGCGTTAATCGGAATTAATCGGCGT 561
Db 223 TCTGTGCCAGCAGCCCGGTAAATACAGAGGATGCAAGCGTTATCCGGNAATGATTTGGCGT 282
QY 562 AAAGCGTCGCGAGCGGTTTTCGAAGTGTGTGAAGCCCGCGCTCAACCTCGGAAC 621
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QY 622 GCATTTGGAGACTGCAAGACTAGTGTGTCAGAGGGGGGTAGAAATTCGCGTGTAGCAG 681
Db 343 GCGGTGGAAACTAACACGCTTGTAGTACGTTAGGGGACAGAGGAATTTCCGGTGGAGCGG 402
QY 682 TGAATGCGTAGAGATGCGGAGGAATACCGATGGCGAAGCGCCCTCGGGATGACACT 741
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QY 742 GACGCTCATGCAAGAAAGCGTGGGAGCAAAACAGGATTAGATACCTGTGTAGTCCAGCC 801
Db 463 GACACTGAGAGACGAAAGCTAGGGAGCGAATGGGATTAGATACCCAGTAGTCTTAGCC 522
QY 802 CTAACGATGTCAATTTAGCTGTGGGGTTTGAATCCTTG--GTAGCGTAGCTTAACCGCT 859
Db 523 GTAACGATGGATACTAGCGCTGTGCGTATCGACCCGTGCGAGTGTGTAGCTTAACCGCT 582
QY 860 GAAATTTGACCGCTTGGGAGTAGTACGGCGCAAGGTTAAAACTCAAGAGAAATTCAGCGGGAC 919
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Db 643 CCGCAACAGCGGTGAGCATGTGGTTTAAATTCATGCAAAAGCGAAGAACTTACCGAGGC 702
QY 980 TTGACATGTACCGAACTTGTGTAGAGATATCTTGGTGGCCCGGAGGCGGTAAACAGG 1039
Db 703 TTGACATGCGGAAATCCTCTTTGAAAGAGAGAGGGGTGCC--TTGCGGAACCGGACACAGG 760

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Qy 1040 TGCTGATGGCTGCTCAGCTCGTGTCTGAGATGTTGGTTAAGTCCCGCAACGAGCG 1099
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Qy 1100 CAACCCCTTGTCATTAAGTTGCCATCATTTAGTTGGGCACTCTAATAGACTGCCGGTGACA 1159
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Db 821 CAACCCCTCGTGTAGTTGGCCACCGTTGAGTTTGGAAACCTGAACAGACTGCCGGTGATA 880
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Qy 1160 AACCGAGGAGGTGGGGATGACGTCGAAGTCTCTCATGGCCCTTATAGACGAGGGCTTCACA 1219
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RESULT 6
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LOCUS BONKF40TR BO 1.6.2_KB tot Brassica oleracea genomic clone BONKF40,
DEFINITION genomic survey sequence.
ACCESSION BZ447500
VERSION BZ447500.1 GI:26712943
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
REFERENCE 1 (bases 1 to 1053)
AUTHORS Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
TITLE Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis
JOURNAL Genome Res. 15 (4), 487-495 (2005)
PUBMED 15805490
COMMENT Other_GSSs: BONKF40TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
FEATURES
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location/Qualifiers
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total DNA inserted into pHD1 using BstXI linkers"

ORIGIN
Query Match 42.6%; Score 613.8; DB 11; Length 1053;
Best Local Similarity 76.0%; Pred. No. 2.4e-177;
Matches 819; Conservative 1; Mismatches 229; Indels 28; Gaps 4;

Qy 222 GCCGACGTCTGATTAGCTAGTTGGTGAGGTGAAGAGCTCACCAAGCGGACGATCAGTAGCG 281
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991 GGTCCGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCACAGACTCTCTACGGGAGG 932
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342 CACGAGTGGGGAATTTTGGACRAATGGGGCAACCCCTGATCCAGCCATGCCCGGTGTCTGA 401
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931 CAGCAGTGGGGAATTTTCCG-CAATGGCGGAAGCCCTGA CGAGCAATGCCCGGTGGAGGT 873
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402 AGAAGCCCTTCGGGTGTAAAGGACTTTTGTTCAGGGAGGAAATCCCGCTGTGTTAATACCC 461
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462 GGGGGGATGACAGTAGTACCBGAAGAAATAAGCACCGGTAACTACTGTCGCACAGCCGCGGT 521
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762 TGGGAGCAAAACAGGATTAGATACCTCTGGTAGTCCAGCCCTTAAACGATGCTAATTAGCT 821
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LOCUS BZ431523 1010 bp DNA linear GSS 13-DEC-2002
DEFINITION BONHD88TF BO 1.6-2 KB tot Brassica oleracea genomic clone BONHD88,
genomic survey sequence.
ACCESSION BZ431523
VERSION BZ431523.1 GI:26677909
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
REFERENCE 1 (bases 1 to 1010)
AUTHORS Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
Uttterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
TITLE Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis
JOURNAL Genome Res. 15 (4), 487-495 (2005)
PUBMED 15805490
COMMENT Other GSSs: BONHD88TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
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total DNA inserted into pHOs1 using BstXI linkers"
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QY 292 GATGATCCGCGCACACTGGGACTGAGACACGCGCCAGACTCTCTACGGAGGCGACAGTGGG 351
DB |||||
950 GATGATCAGCCACACTGGGACTGAGACACGCGCCAGACTCTCTACGGAGGCGACAGTGGG 891
QY 352 GAATTTTGACATGGGGCAACCTGTATCCAGCCATGCGCGTGTCTGAGAAAGCCCTT 411
DB |||||
890 GAATTTTCCGCAATGGCGCAAAACCTTGACGAGCAATGCGCGTGGAGGTAGAAGGCCCTA 831
QY 412 CGGGTTGTAAGGACTTTTGTCAAGGAGGAATCCCGCTGGTTAATACCGCGGGGATG 471
DB |||||
830 CGGGTCTGAACCTCTTTTCCAGAGAAGAA-----GCAATG 794
QY 472 ACAGTACCCBGAAGATAAGCACCGGCTAACTAGTGCAGCAGCCCGGTAATACGTAGG 531
DB |||||
793 ACGGTATCTGGGGAATAAGCATCGGCTAACTCTGTGCCAGCAGCCGCGTAATACAGAGG 734
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DB |||||
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QY 592 ATGTGAAGCCCGGGCTCAACTGCGGACCGCATTTGGAGCTGCAAGACTAGAGTGCCT 651
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673 CCGTCAATATCCAGGGGCTCAACCTCGACAGCGGCTGGAACTACCAAGCTTGTAGTCGG 614
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DB 613 TAGGGCGCAGAGGAATTTCCGGTGGAGCGTGAAATGCGTAGAGATCGCAAGAACACCA 554
QY 712 ATGGCGAAGCGAGCCCTCTGGGATGACACTGAGCTCATGCACGAAGCGTGGGGAGCAA 771
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DB 15 GATCCCGCGAGG 4
RESULT 8
LOCUS DU743187
DEFINITION DU743187 1033 bp DNA linear GSS 27-JAN-2006
ASNC1602.b2 HF10_10-07-02 uncultured marine microorganism
HF10_10-07-02 genomic clone HF0010_017B09, genomic survey sequence.
ACCESSION DU743187
VERSION DU743187.1 GI:85753021
KEYWORDS GSS.
SOURCE uncultured marine microorganism HF10_10-07-02
ORGANISM uncultured marine microorganism HF10_10-07-02
REFERENCE 1 (bases 1 to 1033)
AUTHORS DeLong E.F., Preston C.M., Mincer T., Rich V., Hallam S.J.,
Prigard N.U., Martinez A., Sullivan M., Edwards R., Chisholm S.W.
and Karl D.M.
TITLE Comparative genomics reveals ecological trends in stratified
microbial communities in the ocean's interior
JOURNAL Science (2006) In press
COMMENT Contact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus,
Kerrie Barry, Tijana Glavinadelio, David Bruce, Paul Richardson
and Edward DeLong
US DOE Joint Genome Institute
US DOE Joint Genome Institute
2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA
Tel: 617-253-5271
Fax: 617-253-2679
Email: PMRichardson@lbl.gov; delong@mit.edu
North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid
DNA library prepared from marine picoplankton in the less than 1.6

um, greater than 0.22 um fraction. Sample Date: 10/7/2002
Coordinates: 22.45 N, 158 W Depth: 10 m Temperature: 26.4 C
Salinity 35.08 psu Oxygen: 204.6 umol/kg
Class: fosmid ends.

FEATURES
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than 0.22 um fraction"
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from marine picoplankton in the less than 1.6 um, greater
than 0.22 um fraction. picoplankton collected at 10 m
depth on 10/7/2002. Coordinates: 22.45 N, 158 W. Sample
Date: 10/7/2002 Coordinates: 22.45 N, 158 W Depth: 10 m
Temperature: 26.4 C Salinity 35.08 psu Oxygen: 204.6
umol/Kg"

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ORIGIN

Query Match	41.9%;	Score 602.8;	DB 14;	Length 1033;
Best Local Similarity	78.9%;	Pred. No. 5.9e-174;		
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Qy	528	TAGGGTGCAAGCGTTAAATCGGAATTACTGGCGGTAAAGCGGTGCACAGCGGTTTTGCAAG	587	
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Qy	230	ACGGAAGAGAGAAATGGAATTCCCAGTGTAGAGGTGAAATTCGTAGATATTTGGGAAGAAC	289	
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Qy	708	ACCGATGGCGAAGGAGCCCCCTGGGATGACACTGACGCTCATGCAAGAAAGCTGGGGA	767	
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Qy	828	GGTTTGAACTCCTTGTTAGCGGTAGCTAAACCGGTGAAATTTGACCGCTGGGGAGTAGCGCCG	887	
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Qy	529	ATTTCGACCAACGGCGACAACCTTACAGCCCTTGACATGGGATCGCGAGAGTGGAGA	588	
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Qy	1006	TATCTTGGTGGCCGAAAGGGAGCCGTAAACAGAGTGTGCAATGGCTGTCGTCAAGCTCGTG	1065	
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Qy	589	CACACCTCTTCAGTTTCGGCTGATCCCCACACAGGTGCTGCATGGCTGTCGTGAGTCTG	648	
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Db	829	GGCAGCGACCTTCGGGAGGGAAGCAATTCGTGAAAGCCGCTCTCAATTCGATTGTACT	888
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Qy	1364	AATACGTTCCGGGCTTTGTACACACCGCCGTCACACCAT - GGGAGTGAAGTTTCACCAG	1422
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Db	1009	AACGGGGCGCTTA	1022

RESULT 9					
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DEFINITION	BONDZ28TF BQ 1..6.2 KB tot Brassica oleracea genomic clone BONDZ28, genomic survey sequence.				
ACCESSION	BZ426201				
VERSION	BZ426201.1	GI:26667713			
KEYWORDS	GSS.				
SOURCE	Brassica oleracea				
ORGANISM	Brassica oleracea				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Brassicales; Brassicaceae; Brassica. (bases 1 to 1016)				
AUTHORS	Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Unterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.				
TITLE	Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis Genome Res. 15 (4), 487-495 (2005)				
JOURNAL					
PUBMED	15805490				
CONTACT	Other GSSs: BONDZ28TR Contact: Chris Town				

```

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

FEATURES             Location/Qualifiers
     1..1016
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total DNA inserted into pHOS1
BstXI; 1.6-2 kb sheared
using BstXI linkers"

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ORIGIN		Query Match		Score 602.4;		DB 11;		Length 1016;	
		Best Local Similarity 76.7%;		Fred. No. 7.7e-174;					
		Matches 798;		Conservative 1;		Mismatches 213;		Indels 28; Gaps 4	
Qy	222	GCCGACGTC	TGATTAGCTAGT	TGCTGGGTGAAGT	AGCTCACC	AAAGCGCAGAT	TCAGTACGG	281	
Db	1014	GCTGCGTCT	GATTAGCTAGT	TGCTGGGTGAGGCAAT	AGCTTTACCAAGCGCAT	GATTCAGTACGT	955		


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Qy 282 GGTCTGAGAGATGATCCGCCACACTGGGACTGAGACACGGCCAGACTCTTACGGAGG 341
Db |||
Qy 954 GGTCCGAGAGATGATCAGCCACACTGGGACTGAGACACGGCCAGACTCTTACGGAGG 895
Db |||
Qy 342 CACAGTGGGAAATTTGGCAATGGGGCAACCTTATCCAGCCATCGCGTGTCTGA 401
Db |||
Qy 894 CACAGTGGGAAATTTCCG-CAATGGCGAAAGCCTGACGGAGCAATCGCGTGGAGGT 836
Db |||
Qy 402 AGAAGGCCTTCGGGTGTAAAGGACTTTTGTTCAGGGAGGAAATCCCGCTGGTTAATACCC 461
Db |||
Qy 835 AGAAGGCCTTCGGGTGTAAAGGACTTTTGTTCAGGGAGGAAATCCCGCTGGTTAATACCC 795
Db |||
Qy 462 GCGGGGATGACAGTACBGAAGATAAGCACCGGTAACTACGTGCCAGACGCCCGGT 521
Db |||
Qy 794 ----GCAATGACGGTATCTGGGAAATAAGCATCGGCTAACTCTGTGCGACAGCCCGGT 739
Db |||
Qy 522 AATACGTAGGCTGACAGCTTAATCCGAATTAATCTGGCGTAAAGCGTGGCAGCGGTTT 581
Db |||
Qy 738 AATACAGAGGATGAAGCGTTATCCGGAATGATTGGGCGTAAAGCGTGTGTAGGTGGCTT 679
Db |||
Qy 582 TGCAAGTCTGATGTGAAGCCCGGGCTCAACCTGGGAACGGCATTTGGAGACTGCAAGAC 641
Db |||
Qy 678 TTAAAGTCCCGCTCAATCCAGGGCTCAACCTGGACAGGCGGTGGAACACTACCAAGC 619
Db |||
Qy 642 TAGAGTGGCTCAGAGGGGGTGAATTCCTCGGTGTAGCAGTGAATTCGTGAGATGCGG 701
Db |||
Qy 618 TTGAGTACGTTAGGGGAGAGGGAAATTTCCGTTGGAGCGGTGAATTCGTTAGATCGGA 559
Db |||
Qy 702 AGGAATACCGATGCGGAGGACGCCCTTGGGATGACATGACGCTCATGACGAAAGCG 761
Db |||
Qy 558 AAGAACCAACAGCGGGAAGCACTCTGCTGGGCGGACACTGACACTGAGAGACGAAAGCT 499
Db |||
Qy 762 TGGGGAGCAACAGGATTAGATACCTCTGGTGTAGTCCAGCCCTAAACGATGTCAATTAGCT 821
Db |||
Qy 498 AGGGAGCGAATGGATAGATACCCAGTAGTCTTAGCGTAAACGATGATAGG 439
Db |||
Qy 822 GTTGGGGTTTGAATCTCTTG-GTAGCGTAGTAAACCGGTGAATTAACCGCTGGGGAG 879
Db |||
Qy 438 GCTGTGCTATCGACCGCTGCAGTGTGTAGCTTAACGCGTTAAGTATCCCGCTGGGGAG 379
Db |||
Qy 880 TAGGCGCGCAAGTTAAACTCAAGGATTTGACGGGGACCCGCCACAGCGGTGGATGAT 939
Db |||
Qy 378 TAGCTTCGCAAGAAATGAACTCAAGGAAATTTGACGGGGGCGGCCACAGCGGTGGAGCAT 319
Db |||
Qy 940 GTGGATTAATTCGATGCAACGCGGAAACCTTACCTGCTTGCACATGTACGGAACCTGG 999
Db |||
Qy 318 GTGGTTAATTCGATGCAAGCGAGAACCTTACGAGGGCTTGACATGCGCGAATCCTC 259
Db |||
Qy 1000 TAGAGATATCTTGGTCCCGGAAAGGAGCGCGTAAACAGGTGCTGATGCTGTCTGCTAG 1059
Db |||
Qy 258 TTGAAAGAGAGGGGTGCC--TTCCGGAAACGCGGACACAGGTGTGATGGCTGCTGCTAG 201
Db |||
Qy 1060 CTCGTGCTGAGATGTTGGGTTAAGTCCCGGAAACGAGCGCAACCTTGTCTATTAGTTGC 1119
Db |||
Qy 200 CTCGTGCCGTGAAGGTGTGGGTTAAGTCCCGGAAACGAGCGCAACCTTGTCTATTAGTTGC 141
Db |||
Qy 1120 CATCATTTAGTTGGGCACCTTAATGAGACTGCGCGGTGACAAACCGGAGGAAGTGGGGAT 1179
Db |||
Qy 140 CACCGTTGAGTTGGAAACCTGCAACAGACTGCGCGGTGATTAAGCCGGAGGAGTGAAGAT 81
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Qy 1180 GACGTCAAGTCTCATGGGCCCTTATGAGCAGGGCTTTCACACGTCATACATAGTTCGGTAC 1239
Db |||
Qy 80 GAGCTCAAGTTCATGATGCCCTTATGCCCTGGGCGACACAGCTACTACAAATGGCCGGAC 21
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Qy 1240 AGAGGCTCGTAGCCGCGA 1259
Db |||
Qy 20 AAAGGGTTCGCGATCCCGCGA 1
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RESULT 10

CK280527

LOCUS

DEFINITION

CK280527 889 bp mRNA linear EST 02-AUG-2004
EST743249 Nicotiana benthamiana mixed tissue cDNA library.

normalized, full-length Nicotiana benthamiana cDNA clone NBMA117 5'
end, mRNA sequence.
CK280527
CK280527.1 GI:39850196
EST.
Nicotiana benthamiana
Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 889)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H., and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST743250
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ART TAG GTG ACA CTA TAG.

FEATURES

source

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/clone="NBMA117"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH108-TonA"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN

Query Match 41.6%; Score 599.4; DB 5; Length 889;
Best Local Similarity 81.8%; Pred. No. 6.3e-173;
Matches 727; Conservative 1; Mismatches 158; Indels 3; Gaps 3;
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Db 1 GTTTGATCATGCTCAGATTGAACGCTGGCGGAGCCCTAAACACATGCAAGTCGAGCGGC 60
Qy 67 AACA-GGGTGCTTGCAACC-GCTGACAGTGGCGCAACGGGTGAGTAAATGCGTCCGAATGTA 124
Db 61 AGCAGGGTACTTGTACCTGGTGGCGAGCGCGGCTGAGTAACTGCTAGGAATCTG 120
Qy 125 CCGTGTAAATGGGGATAGCTCGCGGAAACCCGGATTAATACCGCATACGCCCTGAGGGGG 184
Db 121 CCTGTGTAGTGGGGGATAACGCTCGGAAACGGACGCTTAATACCGCATACGCTCCCTACGGGAG 180
Qy 185 AAAGCGGGGATCGAAAGACCTCGGTTATACGACGCGCGACGCTGATATTAGCTAGTTTG 244
Db 181 AAAGCAGGGGACCTTCGGGCGCTTCGCTATCAGATGAGCCTAGGTCGGAATTAGCTAGTTG 240
Qy 245 GTGAGGTAAAGAGCTCACCAAGCGCAGATCAGTAGCGGGTCTGAGAGGATGATCCGCCAC 304
Db 241 GTGAGGTAAAGAGCTCACCAAGCGCAGATCCGTAACCTGCTGAGAGGATGATCAGTCAC 300
Qy 305 ACTGGAGCTGAGACACGCGCCAGACTCTCTACGGGAGGACGACGTGGGGAAATTTTGACAA 364
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Db 301 ACTGGAACCTGAGACACGGTCCAGACTCTCCTACGGAGGACGACGATGGGGAATATGGACAA 360
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Db 361 TGGGCGAAAGCCTGATCCAGCCATGCGCGGTGCTGAAGAAGGCTTCGGATGTGAAGC 420
Qy 425 ACTTTTCTCAGGAGGAAATCCCGCTGTTAAATACCGCGGGGATGACAGTACCBGAAG 484
Db 421 ACTTTAAGTTGGGAGGAGGCGAGTTACCTAAATACGTGATGTTGTTTACGTTACCGACAG 480
Qy 485 AATAAGCACCGGCTAACTAGCTGCGACGACCGCGGTAAATACGTAGGCTGCAAGCGTTAA 544
Db 481 AATAAGCACCGGCTAACTCTGTGCGACGACCGCGGTAAATACAGAGGTGCAAGCGTTAA 540
Qy 545 TCGGAATTAATCGGCGTAAAGCGTGCAGCGCGGTTTTGCAAGTCTCATGTGAAGCCCC 604
Db 541 TCGGAATTAATCGGCGTAAAGCGCGGTAGTGGTGTGTTTAAAGTTGATGTGAATAATCCCC 600
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Db 601 GGGCTCAACCTGGGAACCTGCATCCAAACTGGCAAGCTAGAGTATGTTAGAGGGTGGTG 660
Qy 665 AATTCCCGGTGACGAGTAAATCGTAGAGATCGGAGGAATAACCGATGGCGAAGGCAG 724
Db 661 AATTTCCTGTAGCGGTGAAATCGGTAGATATAGGAAGGACACCAAGTGGCGAAGCGGA 720
Qy 725 CCCCCTGGGATGACACTGACGCTCATGCAAGAGCGTGGGAGCAAAACAGGATTAGATA 784
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RESULT 11
LOCUS BH814966/c
DEFINITION BBP15 Maize B chromosome PCR DNA library Zea mays genomic clone
ACCSSION BH814966
VERSION BH814966.1 GI:31249923
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1143)
Cheng, Y.M. and Lin, B.Y.
Cloning and characterization of maize B chromosome sequences
derived from microdissection
Genetics 164 (1), 299-310 (2003)
12750341
Contact: Bor-yaw Lin
Department of Molecular Biology
National Chung Hsing University
250 Kuo Kuang Rd. Taichung 402, Taiwan (ROC)
Tel: 886-4-2285-1885
Fax: 886-4-2287-4879
Email: bylin@dragon.nchu.edu.tw
Insert Length: 1143 Std Error: 0.00
Class: PCR fragment.
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FEATURES

Source

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Best Local Similarity 87.6%; Pred. No. 6.8e-173;
Matches 691; Conservative 0; Mismatches 91; Indels 7; Gaps 3;

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Qy 712 ATGCGGAAGGACGCCCCCTGGGATGACACTGACGCTCATGCACGAAGCGTGGGAGCAA 771
Db 1083 ATGCGGAAGGACGCCCCCTGGGTCAAGATTGACGCTCATGCACGAAGCGTGGGAGCAA 1024
Qy 772 ACAGGATTAGATACCCCTGGTAGTCCACGCCCTAAACGATGTCATTAAGTGTGGGGGTT 831
Db 1023 ACAGGATTAGATACCCCTGGTAGTCCACGCCCTAAACGATGTCATTAAGTGTGGGGTCTT 964
Qy 832 TGAATCCTTGGTAGCTAGCTAACCGGTGAATTTGACCGCTGGGAGTACGGCGCAAG 891
Db 963 AATTGACGTTGTAACGAGCTAACCGGTGAAGTAGACCGCTGGGAGTACGGTCCGAAG 904
Qy 892 GTTAAAACTCAAAGGAATTGACGGGACCGCCACAAGCGGTGATGATGGATTAAATTC 951
Db 903 ATTAAAACTCAAAGGAATTGACGGGACCGCCACAAGCGGTGATGATGGATTAAATTC 844
Qy 952 GATCAACCGCAAAAACCTTACCTGCTCTTGAATGATGACGAACTTGGTAGAGATATCTT 1011
Db 843 GATCAACCGCAAAAACCTTACCTACCTTGACATGGCTGGAATCTCTTGAGAGATCAGG 784
Qy 1012 GGTGCGGAAAGGAGCGGTAAACAGGTGCTGCATGGCTGCTGACAGTCTGTCGTGTA 1071
Db 783 AGTGCTCGAAAGAGAACCCAGTACACAGGTGCTGCATGGCTGCTGCTCAGCTCGTGTGTA 724
Qy 1072 GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCTTGTCAATTAGTTGCCATCATTTAGTT 1131
Db 723 GATGTT--GGTTAAGTCCCGCAACGAGCGCAACCTTGTCAATTAGTTGCTACGA-----AA 670
Qy 1132 GGGCACTCTAATGAGACTGCGGTGACAAACCGGAGGAAGGTGGGGAT-ACGTCAAGTCC 1191
Db 669 GGGCACTCTAATGAGACTGCGGTGACAAACCGGAGGAAGGTGGGGAT-ACGTCAAGTCC 611
Qy 1192 TCATGGCCCTTATGACGAGGCTTCACACGCTCATACAATCGTCCGTTACAGAGGTCGCTA 1251
Db 610 TCATGGCCCTTATGGGTAGGGCTTCACACGCTCATACAATCGTTCATACAGAGCGCCCA 551
Qy 1252 AGCCGCGAGGTGGTGCCAATCTCATAAACCGATCGTAGTCCGGATCCGACTCTGCAACT 1311
Db 550 ACCGCGAGGGGAGCTTAATCGCAGAAAGTGTATCGTAGTCCGATTTGATGTCGAAT 491
Qy 1312 CGAGTGGTGAAGTCGGAATCGGTAGTAAATCGCAGATCAGCATGCTCGGTGAATAGTT 1371
Db 490 CGACTGCATGAAGTTGGAATCGGTAGTAAATCGCGGATCAGCATGCTCGCGGTGAATAGTT 431
Qy 1372 CCGGGTCTGTACACACCGCCCGTACACCATGGGAGTGGTTTACACGAGAGTGGTA 1431
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RESULT 12
BH705272

LOCUS	BH705272	1079 bp	DNA	linear	GSS 20-FEB-2002
DEFINITION	BOMKA47TF BO_2_3_KB Brassica oleracea genomic clone BOMKA47,				
	genomic survey sequence.				
ACCESSION	BH705272				
VERSION	BH705272.1	GI:18787746			
KEYWORDS	GSS.				
SOURCE	Brassica oleracea				
ORGANISM	Brassica oleracea				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.				
AUTHORS	Ayale, M., Haas, B. J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S., Uteback, T. R., Wortman, J. R., White, O. R. and Town, C. D.				
TITLE	Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis				
JOURNAL	Genome Res. 15 (4), 487-495 (2005)				
PUBMED	15805490				
COMMENT	Other_GSSs: BOMKA47TR Contact: Chris Town TIGR				
	9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523 Fax: 301-838-0208 Email: cdtown@tigr.org DNA is from a doubled haploid provided by Tom Osborn. Seq primer: TF Class: sheared ends.				
FEATURES	source 1..1079 /organism="Brassica oleracea" /mol_type="genomic DNA" /strain="Tol1000DH3" /db_xref="taxon:37112" /clone="BOMKA47" /clone_lib="BO_2_3_KB" /note="vector: pHOsi; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOsi using BstXI linkers"				
ORIGIN	Query Match Best Local Similarity 41.6%; Score 599; DB 11; Length 1079; Matches 799; Conservative 1; Mismatches 232; Indels 27; Gaps 3; QY 215 ACGAGCGCCGACGCTCTGATTAGCTAGTTGGTGAAGTAAGAGCTCACCAAGGCGACGATC 274 Db 50 AGGAGGGCTCGCGTCTGATTAGCTAGTTGGTGAAGCAATAGCTTACCAGGCGATGATC 109 QY 275 AGTAGCGGCTGAGAGGATGATCCGCCACACTGGGACTGAGACACGGCCACGACTCCTTA 334 Db 110 AGTAGCTGGTCCGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCACGACTCCTTA 169 QY 335 CGGAGGCGACAGTGGGGATTTTGGACATGGGGCAACCTGTATCCAGCATCGGCGG 394 Db 170 CGGAGGCGACAGTGGGGATTTTCCGCAATGGGCGAAAGCCTTACGCGAGCAATGCGCG 229 QY 395 TGTCTGAAGAAGGCCTTCGGGTGTGAAGGACTTTTGTACGGAGGAGAAATCCCGCTGGTT 454 Db 230 TGGAGGTAGAAGGCTACGGGTCTGAACTTCTTTTCCAGAGAGAA----- 277 QY 455 AATACCGCGGGGATGACAGTACCBGAAGAATAAGCACCGGCTTAACACTAGTCCACGAG 514 Db 278 -----GCAATGACGGTATCTGGGGAATAAGCATCGGTAACTCTGTGCCAGCAG 326 QY 515 CC CGGTAAATACGTAGGTCAGACGCTTAATCGGAATTACTTGGCGGTAAAGCGTGGCAG 574 Db 327 CC CGGTAAATACAGAGGATCAAGCGTTATCCGGAATGATTGGCGGTAAAGCGTCTGTAG 386 QY 575 GCGGTTTTCGAAGTCTGATGTGAAGCCCGCGGCTCAACCTGGGAAACGGCATTTGGAGACT 634 Db 387 GTGCGTTTTTAAGTCCCGCTCAATCCAGGGGCTCAACCTCGACAGGCGGTGGAAACT 446 QY 635 GCAAGACTAGAGTCCGCTCAGAGGGGGGTGAAGATTTCCGCGTGTAGCTAGTAATGCGGTAGA 694 				

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	umol/kg"
ORIGIN	
Query Match 41.4%; Score 595.8; DB 14; Length 976;	
Best Local Similarity 79.9%; Pred. No. 8.3e-172;	
Matches 739; Conservative 0; Mismatches 182; Indels 4; Gaps 3;	
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DB	926 GGGCCAGCAGCGGGGTATTACGGGGGGTACGAACGTTATTGGAAATTCCTGGGGTAAAA 867
QY	565 GCGTGCACGCGGTTTTCGAAGTCTGATGTGAAGCCCGGGCTCAACCTGGGAACGGC 624
DB	866 GCGGGGTAGCGGTTTCGTTAAGTGGAGTGGAAGCCCGGGCTACCTGGGNAAGCC 807
QY	625 ATTGGAGACTGCRAAGACTAGAGTCGTCAGAGGGGGGTAGAAATTCGCGTGTAGCAGTGA 684
DB	806 TTCCCAACTGGCGAAGTGTGTAGAGGGAAGTGAATTTGTATGTGTAGCGGTGA 747
QY	685 AAT- GCGTAGAGATGCGGAGGATACCGATGGGAGCGGAGCGCCCTGGGATGACACTGA 743
DB	746 AATGGCGTAGATATATCAAGGAATACCAGTGGGAGCGCAGCTTCCTGGACTAACACTGA 687
QY	744 CGCTCATGCAGAAAGCGTGGGAGCAAAAGGATTAGATACCTCGTGTAGTCCACGCGCT 803
DB	686 CGCTAGGTGCGAAGCGTGGGAGCAAAAGGATTAGATACCTCGTGTAGTCCACGCGT 627
QY	804 AAACGATGTCAATTAGCTGTGGGGTTTGAATCCCTTGGTAGCGTAGCTAACGCGTGA 863
DB	626 AAACGATGAGAACTAGCGGTTGGGAGGTTGCGCTCTTAGTGGCGCAGCTAACGCAATAAG 567
QY	864 TTGACCGCTGGGAGTACGCGCCGCAAGGTTTAAACTCAAGGAATTGACGGGACCCGC 923
DB	566 TTCTCCGCTGGGAGTACGCGCCGCAAGGTTTAAACTCAAGGAATTGACGGGAGCCGC 507
QY	924 ACAAGCGGTGATGATGTGGATTAAATTCGATGCAACGCGAAAAACCTTACCTGCTTTGA 983
DB	506 ACAAGCGGTGAGCATGTGTTTAAATTCGATGCAACGCGGAAGACCTTACCACCCCTTGA 447
QY	984 CATGTA CGGAATCTGGTAGAGATATCTTGGTGCCGAAAGGAGCGGTAAACAGGTGCT 1043
DB	446 CATACTCGGAATCTTCTAGAGATAGATTGTTGTCCTTC- GGGAGCCGAGATACAGGTGCT 389
QY	1044 GCATGGCTGTCGTCAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAAGCGCAAC 1103
DB	388 GCATGGCTGTCGTCAGCTCGTGTGAGATGTTGGGTTAAGTCCCGTAAGCGGCAAC 329
QY	1104 CCTTGTCAATTAGTGGCCATC- ATTTAGTTGGGCACTCTAATGAGACTGCCGTTGACAAAC 1162
DB	328 CCTTGTCTTATTTGCCAGCATTCGCTCGGGAATCTAAGGAGACTGCCGTTGACAAAC 269
QY	1163 CGGAGGAAGGTGGGATGACGCTCAAGTCTCATGGCCCTTATGACGAGGCTTACACGT 1222
DB	268 CGGAGGAAGGTGGGACGACGCTCAAGTCTCATGGCCCTTACGGGGTGGGCTACAAACGT 209
QY	1223 CATCAATGGTCGTTACAGAGGGTCGCTTAAGCCGCGAGGTGGTGGCAATCTCATAAACC 1282
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DB 148 TCTCGTAGTCCGATTTGGGTTCTGCAACTCGACCCCATGAAGTCGGAATCGCTAGTAATC 89	
QY 1343 GCGATCAGCATGCTCGGTTGATAGTTCCTCCGGGCTTTGTACACACCGCCGCTCACACC 1402	
DB 88 GCGAATCAAGATGTCGCGGTGAATACGTTCCCGGGCCTTTGTACACACCGCCGCTCACACC 29	
QY 1403 ATGGGAGTGAGTTTACCAAGAGTG 1427	
DB 28 ATGGAAGTGAGTTGCACCAAGAGTG 4	
RESULT 14	
CK280528	
LOCUS 884 bp mRNA linear EST 02-AUG-2004	
DEFINITION EST743250 Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length Nicotiana benthamiana cDNA clone NEM117 5' end, mRNA sequence.	
ACCESSION CK280528	
VERSION CK280528.1 GI:39850200	
KEYWORDS EST.	
SOURCE Nicotiana benthamiana	
ORGANISM Nicotiana benthamiana	
REFERENCE Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B., Staskawicz,B., Jin,H. and Baker,B. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana. 1 (bases 1 to 884)	
AUTHORS Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B., Staskawicz,B., Jin,H. and Baker,B.	
TITLE Generation of EST sequences from Nicotiana benthamiana	
JOURNAL Unpublished (2003)	
COMMENT Other ESTs: EST743249	
Contact: Robin Buell	
The Institute for Genomic Research	
9712 Medical Center Dr, Rockville, MD 20850, USA	
Email: potato-array@tigr.org	
Clones can be requested from the University of Arizona Genomics Institute via http://genome.arizona.edu/orders/	
Seq primer: CAG GAA ACA GCT ATG ACC.	
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/lab_host="DHI08-Tona"	
/clone_lib="Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length"	
/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Nicotiana benthamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."	
ORIGIN	
Query Match 41.2%; Score 592.8; DB 5; Length 884;	
Best Local Similarity 81.6%; Pred. No. 6.8e-171;	
Matches 721; Conservative 1; Mismatches 159; Indels 3; Gaps 3;	
QY	7 GTTTGATCCTCGGCTCAGATTGAACGCTGGCGGATGCTTTACATCATGCAAGTCGAACGGT 66

```
Db 1 GTTTCATCATGGCTCAGATTGAACGCTGGCGGAGCGCTTAACACATGCAAGTCGACGCGC 60
Qy 67 AACACGGTCTTGACACC-GCTGACGAGTGGCGAACGGGTGAGTAATGCTCGGAAATGTA 124
Db 61 AGCACGGGTACTTGTACTCTGTTGGCGAGCGCGGAGTGAATGCTCTAGAAATCTG 120
Qy 125 CCGTGTAAATCGGGGATAGCTCGGGGAGCAAGCCGGAATTAATACCGATACGCGCTTGAGGGG 184
Db 121 CCTGTAGTGGGGGATAACGCTCGGAAACGGAGCGCTAATACCGCATACGTCCTACGGGAG 180
Qy 185 AAAGCGGGGATCGAAAGACCTCGCGTTATACGAGGAGCGAGCTCTGATTAGCTAGTTG 244
Db 181 AAAGCAGGGGACCTTCGGGCTTTCGCTATCAGATGAGCCCTAGTTCGATAGCTAGTTG 240
Qy 245 GTGAGGTAAGAGCTCAACCAAGGCGACGATCAGTAGCGGGTCTCAGAGGAGTATCCGCGCAC 304
Db 241 GTGAGGTAATGGCTCAACCAAGGCGAGCATCCGTAACCTGTCTCAGAGGATGATCATGTCAC 300
Qy 305 ACTGGGACTGAGACACGGCCAGACTCTCTACGGGAGCGACGAGTGGGGAATTTTGGACAA 364
Db 301 ACTGGAACTGAGACACGGTCCAGACTCTCTACGGGAGCGACGAGTGGGGAATATTGGACAA 360
Qy 365 TGGGGGCAACCCCTGATCCAGCCATGCGCGTGTCTGAAGAGCGCTTCGGGTTGTAAGG 424
Db 361 TGGCGAAAGCCCTGATCCAGCCATGCGCGTGTGTGAAGAGGCTCTTCGGATTGTAAGC 420
Qy 425 ACTTTTGTTCAGGGAGGAAATCCCGCTGGTTAATACCGCGGGGATGACAGTACCCGAAAG 484
Db 421 ACTTTAAGTTGGGAGGAGGAGTACCTAATACCTGATTGTTTGGACGTTACCGACAG 480
Qy 485 AATAAGCACCGGCTAATCAGTCCGAGAGCGCGGTAATACTAGAGGTGCAAGCGTTAA 544
Db 481 AATAAGCACCGGCTAATCAGTCCGAGAGCGCGGTAATACTAGAGGTTGCAAGCGTTAA 540
Qy 545 TCGGAATTAATCTGGCGTAAAGCTGCGGAGCGGTTTTCGAACTCTGATGTGAAGCGCC 604
Db 541 TCGGAATTAATCTGGCGTAAAGCGCGGTTGTTTGAAGTGGATGTGAAGTGAATCCCC 600
Qy 605 GGCTCAACCTCGGAAACGGCATTTGGAGACTGCAAGACTAGAGTGCCTCAGAGGGGGTAG 664
Db 601 GGCTCAACCTCGGAACTGATCCAAACCTGGCAAGCTAGAGTATGGTAGAGGTTGGTG 660
Qy 665 AATTCGCGTGTAGAGTGAATGCGTAGAGATGCGGAGGAATACCGATGGGGAAGCGAG 724
Db 661 AATTTCTGTGTAGCGGTGAATGCGTAGATATAGGAAGCAACACAGTGGCGAAGCGGA 720
Qy 725 CCGCTGGGATGACATGACGCTCATGACGAAAGCGTGGGAGCAACAGGATTTAGATA 784
Db 721 CCACCTGGGACTGATCTGACACTGAGGTGCGAAAGCGTGGGAGCAACAGGATTTAGATA 780
Qy 785 CCTGTGTAGTCCACGCGCTAAACGATGTCAATTAGCTGTGTGGG-GGTTTGAATCTTGT 843
Db 781 CCTGTGTAGTCCACGCGTAAACGATGTCAACTAGCGTTGGAGCGCTTGAGCTCTAGT 840
Qy 844 AGCGTAGCTAACCGCGTGAATTAACCGCTTGGGAGTACGCGCG 887
Db 841 GGCGAGCTAACGCATTAAGTTAGCGCTTGGGAGTACGCGCG 884
```

RESULT 15
DU476609
LOCUS
DEFINITION
1098415755465 CHORI-243 Ovis aries genomic clone CH243-341M16,
genomic survey sequence.
ACCESSION
DU476609
VERSION
DU476609.1 GI:77265954
KEYWORDS
GSS.
SOURCE
Ovis aries (sheep)
ORGANISM
Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Fecora; Bovidae; Caprinae; Ovis.
REFERENCE
1 (bases 1 to 917)

AUTHORS
TITLE
JOURNAL
COMMENT

Kirkness, E., Shetty, J., de Jong, P., McEwan, J. C., Oddy, H. and
Cockett, N.
Ovine BAC End Sequences from Library CHORI-243
Unpublished (2004)
Other_GSSs: 1098421043133
Contact: Ewen Kirkness
Email: ekirknes@tigr.org
Sequences generated at the J. Craig Venter Institute Joint
Technology Center (JCVCJTC; <http://www.venterlinstitute.org/>).
Original Trace: 1098415755465 Trace FI: gnlfti|919020497
Insert Length: 184000 Std Error: 0.00 row: M column: 16
Seq primer: Sp6
Class: BAC ends.

FEATURES
source

Location/Qualifiers
1..917
/organism="Ovis aries"
/mol_type="genomic DNA"
/strain="Texel breed"
/db_xref="taxon:9940"
/clone="CH243-341M16"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-243"
/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
The CHORI-243 sheep (M) (Ovis aries) BAC library produced
by Pieter de Jong's lab at CHORI
<http://bacpac.chori.org/library.php?id=162>"

ORIGIN

Query Match 41.2%; Score 592.8; DB 14; Length 917;
Best Local Similarity 80.9%; Pred. No. 6.9e-171;
Matches 717; Conservative 1; Mismatches 159; Indels 9; Gaps 2;
Qy 4 AGAGTTTGATCTCGGCTCAGATTGAACGCTGGCGGATCTTTTACACATGCAAGTCGAAC 63
Db 32 AGGTTTGATCTCGGCTCAGATTGAACGCTGGCGGATCTTTTAAACACATGCAAGTCGAAC 91
Qy 64 GGTAAAC-----AGGGTGTCTGACCGCTGACGAGTGGCGACCGGGTGAGTAATGCGT 115
Db 92 GGCAGCAGCACCTAAGCTTGTAGTGGCTGGCGAGTGGCGACCGGGTGAGTAATGCGT 151
Qy 116 CGGAATGTACCTGTAATGGGGATAGCTCGCGAAAGCGGATTAATACCGCATACGCC 175
Db 152 GGAATCTGGCTCTAGAGGGGATTAATCGGGGAAACTCGGGCTAATACCGCATATCT 211
Qy 176 CTGAGGGGAAAGCGGGGATCGAAAGACTCTCGCGTTATACGAGCAGCGACGCTCTGATT 235
Db 212 CTAAGGAGAAAGCGGGGACCGAAAGGCTCTCGCGTGGGGATGAGCTCGCTCCGATT 271
Qy 236 AGCTAGTTGGTAGGTAGAGTCTACCAAGGCGACGATCAGTAGCGGGTCTGAGAGATG 295
Db 272 AGCTAGTTGGTAGGTAAAGGGCTTACCAAGGCGATGATCGGTAGCTGGTCTTGAAGAGCG 331
Qy 296 ATCCGCCACACTGGGACTGAGACACGGCCAGACTCTCTACGGAGGACGAGTGGGGAAT 355
Db 332 ATCAGGCACACTGGGACTGAGACACGGCCAGACTCTCTACGGAGGACGAGTGGGGAAT 391
Qy 356 TTTGGACAATGGGGCAACCTTGATCCAGCCATCGCGTGTCTGAAGAGGCGCTTCGGG 415
Db 392 ATTGGACAATGGGGCAACCTTGATCCAGCAATCGCGTGGGTGAAGAAGGCTTTTCGGG 451
Qy 416 TTGTAAGACATTTTGTTCAGGGAGGAAATCCCGCTGGTTAATACCGCGGGGATGACAG 475
Db 452 TTGTAAGACCTTTTTCAGTGGGGAGAAAGCGATGTGTGAATAGCACATCGTGTGACGT 511
Qy 476 TACCAGGAATAAGCACCGGCTTAATCGTCCAGCAGCGCGGTAAATACGTTAGGGTGC 535
Db 512 TACCTACAGAGAGACCGGCTTAATCGTCCAGCAGCGCGGTAAATACCGAGGGTGC 571
Qy 536 AAGCGTTAATCGGAATTAATCTGGGCGGTAAAGCGTGGCGAGCGGTTTTTCAAGTCTGATGT 595

[illegible]

Search completed: May 24, 2006, 02:54:40
Job time : 7453 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 23, 2006, 22:12:15 ; Search time 980 Seconds
(without alignments)
10244.937 Million cell updates/sec

Title: US-10-678-023a-1

Perfect score: 1439.2

Sequence: 1 tggagagttgtatcctcggtc.....agaagtggtaggtaacgcg 1440

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_8.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*
- 15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1439.2	100.0	1440	14	ADZ14078 Chromobac
2	1169.6	81.3	1610	10	ADB61691 16S rRNA
3	1165.8	81.0	1460	4	AAC86026 16S rDNA
4	1161.6	80.7	1532	2	AAQ26729 16S rRNA
5	1161.6	80.7	1532	10	ADB61686 16S rRNA
6	1160.6	80.6	1460	4	AAC86024 16S rRNA
7	1159.8	80.6	1488	10	ADB61690 16S rRNA
8	1159.8	80.5	1460	4	AAC86022 16S rRNA
9	1159	80.5	1544	10	ADB61693 16S rRNA
10	1159	80.5	110000	3	AAA81490_00
11	1159	80.5	110000	3	AAA81490_02
12	1159	80.5	110000	3	AAA81490_03
13	1159	80.5	110000	3	AAA81489_2
14	1159	80.5	110000	3	AAA81489_6
15	1159	80.5	110000	3	AAA81489_7
16	1159	80.5	172325	3	AAF21613
17	1159	80.5	349980	3	AAF21607
18	1159	80.5	349980	3	AAF21611

C	19	1159	80.5	349980	3	AAF21612	Aaf21612 Neisseria
	20	1159	80.5	349980	3	AAF21544	Aaf21544 Neisseria
	21	1157.6	80.4	1460	4	AAC86021	Aac86021 R. tenuis
	22	1152.6	80.1	1526	2	AAT01866	Aat01866 P. cepacia
	23	1152	80.0	1544	5	AAS11025	Aas11025 Neisseria
	24	1152	80.0	1544	10	ADB61692	ADB61692 16S rRNA
	25	1150	79.9	1459	4	AAC86028	Aac86028 16S rDNA
	26	1149.8	79.9	1478	4	AAC86023	Aac86023 R. purpur
	27	1149	79.8	1458	6	ABA02418	Aba02418 Type B am
	28	1149	79.8	1458	12	ADM32706	Adm32706 AOB Type
	29	1148.8	79.8	1532	2	AAQ64008	Aaq64008 16S rRNA
	30	1148.4	79.8	1426	4	AAC86029	Aac86029 16S rDNA
	31	1147.6	79.7	1464	10	ADB61688	ADB61688 16S rRNA
	32	1147.6	79.7	1485	4	AAC86030	Aac86030 16S rDNA
	33	1146.8	79.7	1535	2	AAV24295	Aav24295 Burkholde
	34	1146.8	79.7	1535	10	ADB61689	ADB61689 16S rRNA
	35	1145.8	79.6	1464	6	ABL40355	Ab140355 Sequence
	36	1145.8	79.6	1474	2	AAT18766	Aat18766 Pseudomon
	37	1145.6	79.6	1477	2	AAZ26285	Aaz26285 16S rDNA
	38	1137	79.0	1485	10	ADB61687	ADB61687 Nucleotid
	39	1135	78.9	1495	6	ABQ78660	Abq78660 Nucleotid
	40	1135	78.9	20844	3	AA81460	Aaa81460 N. mening
	41	1126.8	78.3	1496	12	ADQ16355	Adq16355 Nucleotid
	42	1126.8	78.3	1496	14	AEA01071	Aea01071 Bordetell
	43	1126	78.2	1530	14	ADM12666	Adm12666 Variolovra
	44	1118.6	77.7	1451	4	AAF74542	Aaf74542 Burkholde
	45	1118.6	77.7	1451	10	ABX10819	Abx10819 Burkholde

ALIGNMENTS

RESULT 1

ADZ14078
ID ADZ14078 standard; DNA; 1440 BP.

XX ADZ14078;

XX 16-JUN-2005 (first entry)

XX Chromobacterium suttsuga NRRL B-30655 16S ribosomal DNA.

XX Insecticide; pesticide; biological control agent; 16S ribosomal rRNA;

XX 16S rRNA; cell culture; ds.

XX Chromobacterium suttsuga.

XX US2005074431-A1.

XX 07-APR-2005.

XX 01-OCT-2003; 2003US-00678023.

XX 01-OCT-2003; 2003US-00678023.

XX (MART/) MARTIN P A W.

XX (SHRO/) SHROPSHIRE A D S.

XX (GUND/) GUNDERSEN-RINDAL D E.

XX (BLAC/) BLACKBURN M B.

XX Martin PAW, Shropshire ADS, Gundersen-Rindal DE, Blackburn MB;

XX WPI: 2005-283752/29.

XX GENBANK; AY344056.

XX New biologically pure culture of a strain of Chromobacterium suttsuga sp. nov. possessing insecticidal activity, useful for biocontrol of insect pests.

XX Claim 3; SEQ ID NO 1; 19pp; English.

XX The present invention relates to a biologically pure culture of a strain of Chromobacterium suttsuga sp. nov. The invention also relates to

CC insecticidally active metabolites obtained from the strain of
CC *Chromobacterium suttsuga* sp. nov. The invention is useful for biocontrol
CC of insect pests. The present sequence is the *Chromobacterium suttsuga*
CC NRRL B-30655 16S ribosomal DNA (rDNA).
XX
SQ Sequence 1440 BP; 359 A; 329 C; 460 G; 291 T; 0 U; 1 Other;

Query Match 100.0%; Score 1439.2; DB 14; Length 1440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGAGTTTCATCTCTGGCTCAGATTGAACCTCGCGCATGCTTTACACATGCAAGTCG 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1 TGGAGAGTTTCATCTCTGGCTCAGATTGAACCTCGCGCATGCTTTACACATGCAAGTCG 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 AACGGTAAACGGGTGCTTTGCACCGCTGACGAGTGGCGAAACGGGTGAGTAATGCGTCGGAA 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 TGTACCGTGTAAATGGGGATAGCTCGGCGAAAGCCGGATTAAATACCGCATACGCCCTGAG 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 181 GGGGAAACCGGGGATCGAAAGACCTCGCTTATACGACGACCGACGCTCTGATTAGCTA 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 241 GTTGTGAGGTAAAGAGCTCACCAGGCGACGATCAGTAGCGGGTCTGAGAGGATGATCCG 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 301 CCACACTGGGACTGAGACACGCGCCAGACTCTCTACGGGAGGACGAGTGGGGAATTTTGG 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 361 ACAATGGGGCAACCTCATCCAGCCATGCCCGTCTGTAAGAGGCGCTTCGGTGTCTA 420
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 421 AAGGACTTTTGTACGGGAGGAAATCCCGCTGGTTAATACCCGGCGGGGATGACAGTACCB 480
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 481 GAAGATTAAGCACCGGCTAACTACGTGCCAGCAGCGCGGTAAATACGTAGGGTGCAGCG 540
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 541 TTAATCGGAATTTACTGGGCGTAAAGCGTGCAGCGCGGTTTGCAGGCTCATGTGAAAG 600
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 601 CCCCGGCTCAACCTGGGAAACGGCAATCGAGACTGAGAGTGCCTGAGAGGGGG 660
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 661 GTAGAAATTCGGGTGTAGCAGTGAATGCGGTAGAGATCGGAGGGAATACCGATGCCGAAG 720
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 721 GCAGCCCCCTGGGATGACACTGACGCTCATGCAAAAACGGTGGGGAGCAACAGGATTA 780
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 781 GATACCTGGTGTAGTCCAGCCCTAAACGATGTCAATTAGCTGTTGGGGTTTGAATCCTT 840
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 841 GGTAGCGTAGCTAAACCGTGAATTTGACCGCTGGGGAGTACGGCCGCAAGGTTAAACT 900
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 901 CAAAGGATTTGACGGGGACCCCGCAAGCGGTGGATGATGTGGATTAATTCGATGCAACG 960
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 901 CAAAGGATTTGACGGGGACCCGACAGCGGTGGATGATGATTAATTCGATGCAACG 960
QY 961 CGAAAAACCTTACCTGCTCTTGACATGTACGGAACCTTGGTAGAGATATCTTGGTCCCGA 1020
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1021 AAGGGAGCCGTAAACAGAGGTGCTGATGGCTGCTGATGCTGCTGATGATGTTGGG 1080
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1081 TTAAGTCCCCCAACGAGCGCAACCCCTTGTCTATTAGTTGCCATCATTTAGTTGGCACTCT 1140
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1141 AATGAGACTGCGGTGACAAACCGGAGGAAGTGGGATGACGTCAAGTCTCATGSGCCC 1200
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1201 TTATGACGAGGCTTACACGTCTATCAATGGTCCGTACAGAGGTCGCTAAGCCGGAG 1260
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1261 GTGTGCAATCTCATAAAACCGATCGTAGTCCGGATCGCACTCTGCAACTCGAGTGCCT 1320
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1321 GAAGTCGGAATCGGTAGTAAATCGCAGATCAGCATGCTGCGGTGAATACGTTCCCGGTCT 1380
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1381 TGTACACACCGCCGTCACACCATGGGAGTGAGTTTCACCAAGAGTGGTAGGCTAACC 1440
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 2
ADB61691
ID ADB61691 standard; DNA; 1610 BP.
XX
XX ADB61691;
XX
XX 04-DEC-2003 (first entry)
XX
DE 16S rRNA of *Burkholderia pseudomallei* DNA sequence.
XX
XX enriching mRNA; high quality bacterial mRNA; bacterial gene expression;
KW poly-A tail; mRNA purification; oligo-dT capture;
KW prokaryote mRNA purification; bridging oligonucleotide; targeting region;
KW capture oligonucleotide; prokaryotic 16S rRNA; prokaryotic 23S rRNA;
KW eukaryotic 17S rRNA; eukaryotic 18S rRNA; eukaryotic 28S rRNA;
KW 28S eukaryotic rRNA bridging oligonucleotide; ds.
XX
OS *Burkholderia pseudomallei*.
XX
XX WO2003054162-A2.
XX
PD 03-JUL-2003.
XX
PF 19-DEC-2002; 2002WO-US041014.
XX
XX 20-DEC-2001; 2001US-00029397.
XX
XX (AMBI-) AMBION INC.
XX
XX Murphy GL, Whitley JP;
XX
XX WPI; 2003-663255/62.
XX
XX Depleting or isolating targeted nucleic acids e.g. rRNA, involves using a
PT bridging oligonucleotide comprising bridging region and a targeting
PT region complementary to a targeted nucleic acid, and a capture
XX oligonucleotide.
XX

Claim 4; Page 175; 208pp; English.

This invention relates to a novel method for isolating, depleting or separating a targeted nucleic acid, such as rRNA, from a sample comprising targeted and non-targeted nucleic acids. It effects a way of enriching for non-targeted nucleic acids such as mRNAs. Isolating sufficient quantities of high quality bacterial mRNA is a demanding process which impedes analysis of bacterial gene expression in the presence of host cells. A small percentage of bacterial mRNAs may be poly-A tailed, but these are targeted for degradation and tend to be unstable. As a result, the commonly employed method for mRNA purification with eukaryotic cells, oligo-dT capture, is ineffective. The present invention provides an alternative, more suitable method for mRNA purification from prokaryotes. The method of the invention comprises the incubation of a sample with a bridging oligonucleotide (containing a targeting region) and subsequently incubating with a capture oligonucleotide allowing the isolation of the target from the sample. The method is useful for depleting or isolating targeted nucleic acid, for example rRNA such as prokaryotic 16S or prokaryotic 23S, eukaryotic 17S or 18S or eukaryotic 28S rRNA, from a sample. The rRNA sequence may comprise any one of 64 fully defined sequences as given in the specification. The present sequence is that of a DNA sequence which represents the sequence of 16S rRNA of *Burkholderia pseudomallei* related to the invention.

Sequence 1610 BP; 394 A; 383 C; 514 G; 319 T; 0 U; 0 Other;

Query Match 81.3%; Score 1169.6; DB 10; Length 1610;

Query Match 91.3%; Score 103.0; DE 10; Length 1010;
Best Local Similarity 88.8%; Pred. NO. 0;
Matches 1278; Conservative 1; Mismatches 156; Indels 5; Gaps 1;

DATE RECEIVED /01/77
STANDARD, T-
C, BPP

Qy	1	TGGAGAGCTTTGATCCTCGCTCAGATTGAA	CGCTGGCGCATGCTTTACACATGCAAGTCG	60
Db	59	TGAGCAGTTGATCCTGGCTCAGATTGAA	CGCTGGCGCATGCTTTACACATGCAAGTCG	118
Qy	61	AACGGTAAACAGGGTGCTTGGCACCCCTGAC	AGAGTGGCGAAACGGGTGAGTAAATGCGTTCGGA	120
Db	119	AACGGCAGCACGGGCTTCGGGCTTCGGCTTC	GGCGAGTGGCGAAACGGGTGAGTTATACATCGGAG	178
Qy	121	TGTACCGTGTAAATGGGGGATAGCTCGGGGA	AAGCGGATTAATACCGCATACGCCCTCGAG	180
Db	179	CATGTCCTGTAGTGGGGGATAGCCCGCGAA	AGCCGAAATTAATACCGCATACGATCTGAG	238
Qy	181	GGGGAAACGGGGGATCCAAAGACCTCGCGT	TATACGAGCAGCCGACGCTCTGATTAGCTA	240
Db	239	GATGAAACGGGGACCTTCGGGCTTCGCGCTA	TAGGTTGGCGCATGCTGATTAGCTA	298
Qy	241	GTGGTGAGGTAAAGAGCTCAACCAAGGCGA	CGATCAGTAGCGGGTCTGAGAGGATGATCCG	300
Db	299	GTGGTGGGGTAAAGGCCCTCAACCAAGGCGA	CGATCAGTAGCTGGTCTGAGAGGACGACCAAG	358
Qy	301	CCACACTGGGACTGAGACACGGCCAGACTCT	TACGGGAGGCACGATGGGGAAATTTTGG	360
Db	359	CCACACTGGGACTGAGACACGGCCAGACTCT	TACGGGAGGCACGATGGGGAAATTTTGG	418
Qy	361	ACAATGGGGCAACCTTGATCCAGCCATCGG	CGGTGCTGAAGAAGGCGCTTCGGGTTGTA	420
Db	419	ACAATGGGCGCAAGCCCTGATCCAGCAATG	CCGCGTGTGTGAAGAAGAGCCCTTCGGGTTGTA	478
Qy	421	AAGGACTTTTGTACAGGAGGAGAAATCCCG	CTGTTTAATACCGGCGGGGATGACAGTAGTACCB	480
Db	479	AAGGACTTTTGTCCGGAAAGAAATCATTTCT	GGCTTAATACCGGAGTGGATGACCGGTACCG	538
Qy	481	GAAGAAATAGCACCGGCTAATCTAGTGCAG	CAGCCGGGTAAATACGTAGGGTCCAAAGCG	540
Db	539	GAAGAAATAGCACCGGCTAATCTAGTGCAG	CAGCCGGGTAAATACGTAGGGTCCGAGCG	598
Qy	541	TTAATCGGAATTACTTGGGCGTAAAGCGTG	CGCAGCGGTTTTCGAAGTCTGATCTGAAAG	600
Db	599	TTAATCGGGATTACTTGGGCGTAAAGCGTG	CGCAGCGGTTTTCGAAGTCTGATCTGAAAT	658
Qy	601	CCCGGCGCTCAACTGGGAAACGGCATTTGG	AGACTGCAAGACTAGAGTGCCTCAGAGGGGG	660

PD 28-JUN-2001.
XX
XX PF 28-DEC-2000; 2000WO-AU001611.
XX
XX PR 23-DEC-1999; 99AU-00004867.
XX
XX PA (CRCW-) CRC WASTE MANAGEMENT & POLLUTION CONTROL.
XX
XX FI Hugenholtz P, Crocetti GR, Tyson GW, Blackall LL;
XX
XX DR WPI; 2001-408656/43.
XX
XX PT Novel oligonucleotide probe or primer useful for detecting polyphosphate
XX
XX PT accumulating organism in a sample, comprises a sequence that is unique to
XX
XX PT 16S rDNA of polyphosphate accumulating organisms.
XX
XX PS Claim 4; Fig 3; 54pp; English.
XX
XX CC The sequences given in AAC86021-30 represent 16S rDNA sequences from
XX
XX CC polyphosphate accumulating organisms (PAOs). Sequences which are unique
XX
XX CC to these 16S rDNA sequences are used to create a probe or primer for
XX
XX CC detecting the relevant organisms. The primer/probe sequences are useful
XX
XX CC for detecting PAO cells in a sample, by treating cells in the sample to
XX
XX CC fix cellular contents, contacting fixed cells with the primer/probe which
XX
XX CC is labelled with a radiolabel, a reporter group or a hapten, under the
XX
XX CC conditions which allow the probe to hybridize with 16S rRNA within the
XX
XX CC fixed cell, removing unhybridized probe from the fixed cells, and
XX
XX CC detecting the labeled probe-RNA hybrid by fluorescence in situ
XX
XX CC hybridization. The primer/probe sequences are useful for identifying PAOs
XX
XX CC that are capable of biologically removing phosphorus from waste water.
XX
XX CC Rapid assessment of the presence of a number of PAOs in a waste water
XX
XX CC sample, can be done using the primer/probe sequences. They allow quick
XX
XX CC and convenient assessment of whether a sludge or waste water sample
XX
XX CC includes PAOs and allows quantitation of PAO cells in samples. (Updated
XX
XX CC on 06-AUG-2003 to correct OS field.)
XX
XX SQ Sequence 1460 BP; 359 A; 338 C; 475 G; 288 T; 0 U; 0 Other;
Query Match 81.0%; Score 1165.8; DB 4; Length 1460;
Best Local Similarity 89.3%; Pred. No. 0;
Matches 1267; Conservative 1; Mismatches 149; Indels 2; Gaps 1;
QY 24 ATTGAACCTGCGCGCATCTTACACATGCAAGTCGAACGCTACACGSGTCTTGACAC 83
DB 1 ATTAACCGTGGCGGCATCGCCTTACACATGCAAGTCGAACGCGACACGGGGCAACCT 60
QY 84 GCTGACGAGTGGCGAACGGGTGAGTAATCGCTCGGAATGTACCGTGTAAATGGGGATAGC 143
DB 61 GGTGGGAGTGGCGGACGGGTGAGTAATGTCATCGGAACGTGCCCTGAAGTGGGGATAAC 120
QY 144 TCGGCGAAAGCCGGATTATACCGCATACGCCCTGAGGGGGAACGGGGGATCGAAAGA 203
DB 121 GCAGCGAAAGCTACGCTAATACCGCATATCTGTGAGCAGGAAAGCAGGGGATCGCAAGA 180
QY 204 CCTCGGTTATACGAGCGCCACGCTGTGATTAGCTAGTGTGAGGTAAAGCTCACCA 263
DB 181 CCTTGGCTTTGGGAGCGCCGATGTCGGATTAGCTAGTGTGGGGTAAATGGCCATCCA 240
QY 264 AGCGCACCATAGTAGCGGGTCTGAGAGGATGATCCGCCACACTGGGACTGAGACACGGC 323
DB 241 AGCGCACCATCGTAGCGGGTCTGAGAGGATGATCCGCCACACTGGGACTGAGACACGGC 300
QY 324 CCAGACTCTACGGAGGCGAGTGGGGAATTTGGACAATGGGGGCAACCCCTATCCA 383
DB 301 CCAGACTCTACGGAGGCGAGTGGGGAATTTGGACAATGGGGGCAACCCCTATCCA 360
QY 384 GCCATGCGCGTGTCTGAAGAAGGCTTCGGGTGTGAAAGGACTTTTGTGACGGAGGAAA 443
DB 361 GCATGCGCGGTGAGTGAAGAAGGCTTCGGGTGTGAAAGCTCTTTTCGGCGGGGAGAAA 420
QY 444 TCCCGTGGTTAATACCCCGCGGGGATGACAGTACCBGAAGAATAAGCAACCGGCTAACTA 503
DB 421 TTGCTTGGGTAAATACCCCTGAGTAGATGACGGTACCCGAAATGAAGAAGCACCGGCTAACTA 480

QY 504 CGTGCCAGCAGCCCGCGTAACTAGTAGGTGCAAGCGTTAATCGGAATTAATCTGGCGGTAA 563
DB 481 CGTGCCAGCAGCCCGCGTAACTAGTAGGTGCGAGCGTTAATCGGAATTAATCTGGCGGTAA 540
QY 564 AGCGTGCAGAGCGGTTTTTGCAGTCTGATGTGAAGACCCCGGCTCAACCTGGGAAACGG 623
DB 541 AGCGTGCAGAGCGGTTTTTGTAGTCAGATGTGAATCCCGGCTCAACCTGGGAACTG 600
QY 624 CATTGGAGACTGCAAGACTAGAGTGCCTCAGAGGGGGTGAATTCGCGGTGTAGCAGTG 683
DB 601 CATTGGAGACTGCAAGACTGGAGTTTGGCAGAGGGGGTGAATTCACGCTGTAGCAGTG 660
QY 684 AAATGCGTAGAGATGCGGAGGAATACGATGGCGAAGCAGCCCTGGGATGACACTGA 743
DB 661 AAATGCGTAGAGATGTGGAGGAACACGATGGCGAAGCAGCCCTGGGCAATACTAGA 720
QY 744 CGCTCATGCGAAGCGTGGGAGCAAAACAGGATTAGATACCCCTGGTAGTCCACGCCCT 803
DB 721 CGCTCATGCGAAGCGTGGGAGCAAAACAGGATTAGATACCCCTGGTAGTCCACGCCCT 780
QY 804 AAACGATGTCAATTAGTCTGTGGGGTTTGAATCC--TTGTAGCGGTAGCTAAACGCGTGA 861
DB 781 AAACGATGTCAACTAGTGTGGGAGGTTAAACCTTTTAGTGCCTAGCTAAACGCGTGA 840
QY 862 AATTGACCGCTGGGAGTAGCGCCGCAAGGTTAAACTCAAAGGAATTGACGGGGACCC 921
DB 841 AGTTGACCGCTGGGAGTAGCGCCGCAAGGTTAAACTCAAAGGAATTGACGGGGACCC 900
QY 922 GCACAAGCGGTGGATGATGTGATTAAATTCGATCAACGCGAAACCTTACCTGCTCTT 981
DB 901 GCACAAGCGGTGGATGATGTGATTAAATTCGATCAACGCGAAACCTTACCTGCTCTT 960
QY 982 GACATGTACGAACTTGGTAGAGATATCTTGGTCCCGAAGGAGCGGTAAACACAGTG 1041
DB 961 GACATGTACGAACTTGGTAGAGATATCTTGGGAGTGTCTGCAAGAGAACTGCAACAGGTG 1020
QY 1042 CTGCATGGCTGCTGCTGCTGCTGAGATGTGGGTAAAGTCCCGCAACGAGCGCA 1101
DB 1021 CTGCATGGCTGCTGCTGCTGCTGAGATGTGGGTAAAGTCCCGCAACGAGCGCA 1080
QY 1102 ACCCTTGTCAATTAGTTGTCATCATTTAGTTGGGCACCTCTAATGAGACTGCCGGTGACAAA 1161
DB 1081 ACCCTTGTCAATTAGTTGTCATCATTTAGTTGGGCACCTTTAATGAGACTGCCGGTGACAAA 1140
QY 1162 CCGAGGAAGGTGGGATGACGTCAAGTCTCATGGCCCTTATGAGCAGGSGTTTACACG 1221
DB 1141 CCGAGGAAGGTGGGATGACGTCAAGTCTCATGGCCCTTATGGGTAGGSGTTTACACG 1200
QY 1222 TCATACATGCTCGGTACAGAGGTCGCTAAGCCGCGAGGTGGTGCCCAATCTCATAAAAC 1281
DB 1201 TCATACATGCTCGGTTCAGAGGTTGCCAACCCCGAGGGGAGGCCAATCTCAGAAAGC 1260
QY 1282 CGATCGTAGTCCGGATCGCACTCTGCAACTCGAGTGCCTGAAGTGGGAATCGCTAGTAAT 1341
DB 1261 CGATCGTAGTCCGGATCGCACTCTGCAACTCGAGTGCCTGAAGTGGGAATCGCTAGTAAT 1320
QY 1342 CGCAGATCAGCATGCTGGCGTGAATACGTTCCGGGTCTTGTACACACCGCCCGTACAC 1401
DB 1321 CGCGGATCAGCATGCGCGGTGAATACGTTCCGGGTCTTGTACACACCGCCCGTACAC 1380
QY 1402 CATGGAGTGAAGTTTCCACAGAAGTGGGTAGGCTTAACCG 1440
DB 1381 CATGGAGCGGGTCTGCGCAGAGTAGTTAGCTTAACCG 1419

RESULT 4
AAQ26729
ID AAQ26729 standard; cDNA; 1532 BP.
XX
XX AC AAQ26729;
XX
XX DT 25-JAN-1993 (first entry)

XX 16S rRNA gene from Bordetella bronchiseptica.
 DE rapid; examine; samples; test; identify; detect; ss.
 XX Bordetella bronchiseptica.
 KW JP04179480-A.
 XX 26-JUN-1992.
 XX 09-NOV-1990; 90JP-00304758.
 XX 09-NOV-1990; 90JP-00304758.
 XX (ZENK-) ZENKOKU NOGYO KYODO KUMIAI REN.
 XX (NISE-) NIPPON SEIHUN KK.
 XX WPI; 1992-263661/32.
 XX 16-Sr-RNA gene of Bordetella bronchiseptica - DNA fragment for probe and
 PT the detection of the gene using them allowing examination of many samples
 PT in short period.
 XX Claim 1; Page 1; l1pp; English.
 XX This sequence represents the 16S rRNA gene from Bordetella
 CC bronchiseptica. The 16S rRNA gene fragment was amplified by PCR and
 CC isolated. The B. bronchiseptica 16S rRNA full-length gene was cloned and
 CC the base sequence was determined. See also AA026730-6
 XX
 SQ Sequence 1532 BP; 378 A; 363 C; 490 G; 301 T; 0 U; 0 Other;
 Query Match 80.7%; Score 1161.6; DB 2; Length 1532;
 Best Local Similarity 88.4%; Pred. No. 0;
 Matches 1273; Conservative 1; Mismatches 161; Indels 5; Gaps 1;
 1 TGGAGAGTTTTCATCTCGCTCAGATTGAACCGCTGGCGCATGCTTTTACACATGCAAGTCG 60
 6 TGAAGAGTTTTCATCTCGCTCAGATTGAACCGCTGGCGCATGCTTTTACACATGCAAGTCG 65
 61 AACGGTAACAGGGTGTCTTGCACCGCTGACAGTGGCGAAACGGGTGAGTAATGCGTCGGAA 120
 66 GACGGCAGCAGCGGCTTCGGCTCGTGGCGAGTGGCGAAACGGGTGAGTAATGATGATCGGAA 125
 121 TGTACCGTGTAAATGGGGATAGCTCGCGAAGCGGATTAATACCGCATACGCCCTGAG 180
 126 CGTCCAGTAGCGGGGATTAACCTACGCGAAGCGTGGCTTAATACCGCATACGCCCTTACG 185
 181 GGGGAAAGCGGGGATCGAAAGACCTCGCGTTATACGAGCAGCGCGATCTGTATTAGCTA 240
 186 GGGGAAAGCGGGGACCTTCGGGCTCGCATATTGGAGCGCGCATATCGGATTAGCTA 245
 241 GTTGGTGAAGTAAGAGTCTACCAAGGCGAAGATCAGTAGCGGGTCTGAGAGGATGATCCG 300
 246 GTTGGTGGGTAAACGGCTTACCAAGGCGAAGATCCGTAGCTGTGGTTGAGAGGACGACAG 305
 301 CCACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGCGCAGTGGGGAATTTGG 360
 306 CCACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGCGCAGTGGGGAATTTGG 365
 361 ACAATGGGGCAACCTTGATCCAGCCATGCGCGTGTCTGAAGAAAGGCGCTTCGGGTTGTA 420
 366 ACAATGGGGCAACCTTGATCCAGCCATCCCGCTGTGCGATGAAGCGCTTCGGGTTGTA 425
 421 AAGCACTTTTGTAGGAGGAAATCCCGTGTGTTAAATACCCGGCGGGGATGACAGTACCB 480
 426 AAGCACTTTTGGCAGGAAAGAAACGGCAGCGGCTTAATATCTGTGCAACTGACGGTACCT 485
 481 GAAGAATAAGCACCAGGCTAACTAGTGCAGCAGCGCGGTAAATACCTAGGGTGCAGCG 540
 486 GCAGAAATAGCACCAGGCTAACTAGTGCAGCAGCGCGGTAAATACCTAGGGTGCAGCG 545

Qy 541 TTAATCGGAATTACTGGCGTAAAGCGTGGCGAGCGGTTTTCGAAGCTCTGATGTGAAG 600
 Db 546 TTAATCGGAATTACTGGCGTAAAGCGTGGCGAGCGGTTTCGGAAGAAGAGATGTGAAT 605
 Qy 601 CCCGGGCTCAACTCTGGGAAACGGCATTTGGAGACTGCAAGACTAGAGTGCCTCAGAGGGG 660
 Db 606 CCCAGGGCTTAAACCTTGGAACTGCAATTTTAACTACCGGCTAGAGTGTGTCTCAGAGGGAG 665
 Qy 661 GTAGAAATTCGCGTGTAGCAGTGAATGCGTAGAGATGCGGAGGAATACCGATGCCGAAG 720
 Db 666 GTGGAATTCGCGTGTAGCAGTGAATGCGTAGATATGCGGAGGAACACCGATGCCGAAG 725
 Qy 721 GCAGCCCTCTGGGATGACACTGACGCTCATGCAAGAAAGCGTGGGAGCAAAACAGGATTA 780
 Db 726 GCAGCCCTCTGGGATGACACTGACGCTCATGCAAGAAAGCGTGGGAGCAAAACAGGATTA 785
 Qy 781 GATACCTCTGTAGTCCACGCCCTTAAACGATGTCAATTAGCTGTGGGGTGTGAATCTTT 840
 Db 786 GATACCTCTGTAGTCCACGCCCTTAAACGATGTCAATTAGCTGTGGGGCTTTCGGGCTT 845
 Qy 841 GGTAGCGTAGCTAACCGCTGAATTTGACCGCTGGGAGTACGCGCCGCAAGGTTTAAACT 900
 Db 846 GGTAGCGTAGCTAACCGCTGAATTTGACCGCTGGGAGTACGCGTCCGAAGATTAAACT 905
 Qy 901 CAAAGGAATTGACGGGACCCGACAAAGCGTGGATGATGTGGAATTAATTCGATGCAACG 960
 Db 906 CAAAGGAATTGACGGGACCCGACAAAGCGTGGATGATGTGGAATTAATTCGATGCAACG 965
 Qy 961 CGAAAAACCTTACCTGCTTTGACATGATACGGAACCTTGGTAGAGATATCTTGGTGCAGA 1020
 Db 966 CGAAAAACCTTACCTGCTTTGACATGATCTGGAATCCGAAGAGATTTGGAGTGTCTCGC 1025
 Qy 1021 AAGGAGCGCTTAACACAGGTGCTGCATGGCTGCTGCAGCTCGTGCAGATGTTGGG 1080
 Db 1026 AAGGAGCGCTTAACACAGGTGCTGCATGGCTGCTGCAGCTCGTGCAGATGTTGGG 1085
 Qy 1081 TTAAGTCCCCCAACGAGCGCAACCTTGTCTATTAGTTGCCATCATTTAGTTGGGCACTCT 1140
 Db 1086 TTAAGTCCCCCAACGAGCGCAACCTTGTCTATTAGTTGCTACGAA-----GGGCACTCT 1140
 Qy 1141 AATGAGACTCCCGGTGACAAACCGGAGGAAGGTGGGATGACGTCAAAGTCTCATGCGCC 1200
 Db 1141 AATGAGACTCCCGGTGACAAACCGGAGGAAGGTGGGATGACGTCAAAGTCTCATGCGCC 1200
 Qy 1201 TTAATGACAGGGCTTCACACGTTCATCAATGTGCTGACAGAGGTCGCTAAGCCGCGAG 1260
 Db 1201 TTAATGAGTGGGCTTCACACGTTCATCAATGTGCTGAGAGAGGTCGCAACCCGCGAG 1260
 Qy 1261 GTGCTGCAATCTCATAAACCCGATCGTAGTCCGGATCGCACTCTGCAACTCGAGTGGT 1320
 Db 1261 GGGAGCCCAATCCAGAAACCCGATCGTAGTCCGGATCGCACTCTGCAACTCGAGTGGT 1320
 Qy 1321 GAAGTGGGAATCGCTAGTAATTCGAGATCAGCATGCTGCGGTGAATACGTTCCCGGTCT 1380
 Db 1321 GAAGTGGGAATCGCTAGTAATTCGAGATCAGCATGCTGCGGTGAATACGTTCCCGGTCT 1380
 Qy 1381 TGTACACACCGCCGCTCACACCATGGAGTGGTTCACAGAGTGGGTGAGCTAACCG 1440
 Db 1381 TGTACACACCGCCGCTCACACCATGGAGTGGTTCACAGAGTGGGTGAGCTAACCG 1440
 RESULT 5
 ADB61686
 ID ADB61686 standard; DNA; 1532 BP.
 XX ADB61686;
 AC
 DT 04-DEC-2003 (first entry)
 XX
 DE 16S rRNA of Bordetella bronchiseptica DNA sequence.
 XX enriching mRNA; high quality bacterial mRNA; bacterial gene expression;
 KW poly-A tail; mRNA purification; oligo-dT capture;

prokaryote mRNA purification; bridging oligonucleotide; targeting region;
capture oligonucleotide; prokaryotic 16S rRNA; prokaryotic 23S rRNA;
eukaryotic 17S rRNA; eukaryotic 18S rRNA; eukaryotic 28S rRNA;
28S eukaryotic rRNA bridging oligonucleotide; ds.

Bordetella bronchiseptica.

WO2003054162-A2.

03-JUL-2003.

19-DEC-2002; 2002WO-US041014.

20-DEC-2001; 2001US-00029397.

(AMBI-) AMBION INC.

Murphy GL, Whitely JP;

WPI; 2003-663255/62.

Depleting or isolating targeted nucleic acids e.g. rRNA, involves using a
bridging oligonucleotide comprising bridging region and a targeting
region complementary to a targeted nucleic acid, and a capture
oligonucleotide.

Claim 4; Page 171-172; 208pp; English.

This invention relates to a novel method for isolating, depleting or
separating a targeted nucleic acid, such as rRNA, from a sample
comprising targeted and non-targeted nucleic acids. It effects a way of
enriching for non-targeted nucleic acids such as mRNAs. Isolating
sufficient quantities of high quality bacterial mRNA is a demanding
process which impedes analysis of bacterial gene expression in the
presence of host cells. A small percentage of bacterial mRNAs may be poly
-A tailed, but these are targeted for degradation and tend to be
unstable. As a result, the commonly employed method for mRNA purification
with eukaryotic cells, oligo-dT capture, is ineffective. The present
invention provides an alternative, more suitable method for mRNA
purification from prokaryotes. The method of the invention comprises the
incubation of a sample with a bridging oligonucleotide (containing a
targeting region) and subsequently incubating with a capture
oligonucleotide allowing the isolation of the target from the sample. The
method is useful for depleting or isolating targeted nucleic acid, for
example rRNA such as prokaryotic 16S or prokaryotic 23S, eukaryotic 17S
or 18S or eukaryotic 28S rRNA, from a sample. The rRNA sequence may
comprise any one of 64 fully defined sequences as given in the
specification. The present sequence is that of a DNA sequence which
represents the sequence of 16S rRNA of Bordetella bronchiseptica related
to the invention.

Sequence 1532 BP; 378 A; 363 C; 490 G; 301 T; 0 U; 0 Other;

Query Match 80.7%; Score 1161.6; DB 10; Length 1532;

Best Local Similarity 88.4%; Pred. No. 0;

Matches 1273; Conservative 1; Mismatches 161; Indels 5; Gaps 1;

1 TGGAGAGTTTGATCTCGGCTCAGATTGAACGCTGCGGCGATGCTTTACACATGCAAGTCG 60
|||||

6 TGAAGAGTTTGATCTCGGCTCAGATTGAACGCTGCGGCGATGCTTTACACATGCAAGTCG 65
|||||

61 AACGGTAACAGGTGCTTGCACCGCTGACGAGTGGCGAACGGTGAGTAATCGTCGGAA 120
|||||

66 GACGCGACGACGGGCTTCGGCTGGTGGCGAGTGGCGAACGGTGAGTAATGATCGGAA 125
|||||

121 TGTACCGTGTAAATGGGGGATAGTCGGCGAAAGCCGGATTAAATACCGATACGCCCTGAG 180
|||||

126 CGTGCCAGTAGCGGGGATTAATACTACGCGAAGCGTGGCTAATACCGCATACGCCCTAGC 185
|||||

181 GGGGAAAGCGGGGATCGAAAGACCTCGCGTTATACGACGACCGACGCTCTGATTAGCTA 240
|||||

186 GGGGAAAGCGGGGACCTTCGGGCTTCGCACTATTGGAGCGCCGATATCGGATTAGCTA 245
|||||

Qy 241 GTTGGTGAAGAGCTCACCAGGCGACGATCAGTAGCGGGTCTCAGAGAGATGATCCG 300
|||||

Db 246 GTTGGTGGGTAAACGGCTTACCAGGCGACGATCCGTTAGCTGGTTTGAGAGGACGACAG 305
|||||

Qy 301 CCACACTGGGACTGAGACACGGCCAGACTCTTACGGGAGGACGACGATGGGGAATTTGG 360
|||||

Db 306 CCACACTGGGACTGAGACACGGCCAGACTCTTACGGGAGGACGACGATGGGGAATTTGG 365
|||||

Qy 361 ACAATGGGGCAACCTTGATCCAGCCATGCGCGTGTCTGAAGAAGGCTTCGGGTTGTA 420
|||||

Db 366 ACAATGGGGCAACCTTGATCCAGCCATGCGCGTGTCCGATGAAGGCTTCGGGTTGTA 425
|||||

Qy 421 AAGGACTTTTGTCAAGGAGGAATCCCGCTGTTAATACCCGCGGGGATGACAGTACCB 480
|||||

Db 426 AAGCACTTTTGGCAGGAAGAAGACGGCAGCGGCTAATATCTGTGCAACTGACCGTACCT 485
|||||

Qy 481 GAAGAATAAGCACCGGCTAACTACGTCCAGCAGCCGCGTAAATACGTAGGTTGCAAGCG 540
|||||

Db 486 GCAGAATAAGCACCGGCTAACTACGTCCAGCAGCCGCGTAAATACGTAGGTTGCAAGCG 545
|||||

Qy 541 TTAATCGGAATTACTGGGCGTAAAGCGTGGCAGCGGTTTTGCAAGTCTGATGTGAAG 600
|||||

Db 546 TTAATCGGAATTACTGGGCGTAAAGCGTGGCAGCGGTTTCGGAAGAAAGATGTGAAT 605
|||||

Qy 601 CCCCGGCTCAACCTGGGAACGCAATTGGAGACTGCAAGACTAGAGTCCGTACAGAGGGG 660
|||||

Db 606 CCCAGGGCTTAACCTTGGAACTGCAATTTTAACTACCGGGCTAGAGTGTGTACAGGGAG 665
|||||

Qy 661 GTAGAATTCCCGTGTAGCAGTGAATCGTGTAGAGATCGCGAGGAATACCGATGGCGAAG 720
|||||

Db 666 GTGGAATTCCCGTGTAGCAGTGAATCGTGTAGATATGCGGAGGAACACCGATGGCGAAG 725
|||||

Qy 721 GCAGCCCTGGGATGACACTGAGCTCATGCAGAAAGCGTGGGCGCAACAGGATTA 780
|||||

Db 726 GCAGCCCTGGGATGACACTGAGCTCATGCAGAAAGCGTGGGCGCAACAGGATTA 785
|||||

Qy 781 GATACCTGTGTAGTCCAGCCCTAAAACGATGCTCAATAGCTGTGGGGTTTGAATCCTT 840
|||||

Db 786 GATACCTGTGTAGTCCAGCCCTAAAACGATGCTCAATAGCTGTGGGGCTTCGGGCTT 845
|||||

Qy 841 GGTAGCTGTAGTAAACCGGTGAATTTGACCGCTGGGAGTACCGCGCAAGGTTAAAACT 900
|||||

Db 846 GGTAGCTGTAGTAAACCGGTGAATTTGACCGCTGGGAGTACCGGTTCGCAAGTTAAAACT 905
|||||

Qy 901 CAAGGAATTACCGGGGACCCGACACAGCGGTGATGATGATGATTAATTCGATGCAACG 960
|||||

Db 906 CAAGGAATTACCGGGGACCCGACACAGCGGTGATGATGATGATTAATTCGATGCAACG 965
|||||

Qy 961 CGAAAAACCTTACCTGTCTTTGACATGTACCGAACTTGGTAGAGATATCTTTGGTGCCCGA 1020
|||||

Db 966 CGAAAAACCTTACCTGTCTTTGACATGTCTGGAATCCCGAAGAGATTTGGGAGTGTCTCGC 1025
|||||

Qy 1021 AAGGAGCGGTAAACACAGGTGCTGATGGCTGTGTGTGCTGAGTCTGCTGAGATGTTGGG 1080
|||||

Db 1026 AAGGAACCGGAAACACAGGTGCTGATGGCTGTGTGTGCTGAGTCTGCTGAGATGTTGGG 1085
|||||

Qy 1081 TTAAGTCCCGCAACGAGCGCAACCTTGTCTATTAGTTGCCCATCATTTAGTTGGGCACCT 1140
|||||

Db 1086 TTAAGTCCCGCAACGAGCGCAACCTTGTCTATTAGTTGTCTAGAAA-----GGGCACCTCT 1140
|||||

Qy 1141 AATGAGACTGCGCGTGAACAAACCGGAGGAGGTGGGATGACGTCAAGTCTCTATGGCCC 1200
|||||

Db 1141 AATGAGACTGCGCGTGAACAAACCGGAGGAGGTGGGATGACGTCAAGTCTCTATGGCCC 1200
|||||

Qy 1201 TTATGAGCAGGGCTTCAACGTCATACAAATGGTTCGGTACAGAGGTGCTTAAGCCGCGAG 1260
|||||

Db 1201 TTATGGGTAGGGCTTCAACGTCATACAAATGGTTCGGGACAGAGGTGCTCCCAACCCGCGAG 1260
|||||

Qy 1261 GTGGTGCCCAATCTCATATAACCGATCGTAGTCCGGATCGCACTCTGCAACTCTAGTGGCT 1320
|||||

Db 1261 GGGGAGCCAAATCCCAAGAAACCGATCTGTAGTCCGGATCGCACTCTGCAACTCTAGTGGCT 1320
|||||

Qy 1321 GAAGTGCGGAATCGCTGTAGTAATTCGAGATCAGCATGCTCGGTGGAATACGTTCCCGGGTCT 1380
|||||

Db 1321 GAAAGTCGGAATCGTAGTAATCGCGGATCGCATGTCGCGGTGAATACGTTCCCGGTCT 1380
Qy 1381 TGTACACACCGCCCGTACACCATGGGAGTGCAGTTTACCAAGAGTGGTAGGTAACCG 1440
Db 1381 TGTACACACCGCCCGTACACCATGGGAGTGGGTTTACCAAGAGTAGTTAGCCTAACCG 1440

RESULT 6

AAC86024
ID AAC86024 standard; cDNA; 1460 BP.

XX AAC86024;

DT 29-AUG-2001 (first entry)

DE R.tenuis 16s rDNA #3.

XX 16S rDNA; polyphosphate accumulating organism; PAO; probe; primer;
KW detection; phosphorus; waste water; sludge; ss.

XX Rhodocyclus tenuis.

XX WO200146459-A1.

XX 28-JUN-2001.

XX 28-DEC-2000; 2000WO-AU001611.

XX 23-DEC-1999; 99AU-00004867.

XX (CRCW-) CRC WASTE MANAGEMENT & POLLUTION CONTROL.

XX Hugenholtz P, Crocetti GR, Tyson GW, Blackall LL;

XX WPI; 2001-408656/43.

XX Novel oligonucleotide probe or primer useful for detecting polyphosphate
PT accumulating organism in a sample, comprises a sequence that is unique to
PT 16S rDNA of polyphosphate accumulating organisms.

XX Claim 4; Fig 3; 54pp; English.

XX The sequences given in AAC86021-30 represent 16S rDNA sequences from
CC polyphosphate accumulating organisms (PAOs). Sequences which are unique
CC to these 16S rDNA sequences are used to create a probe or primer for
CC detecting the relevant organisms. The primer/probe sequences are useful
CC for detecting PAO cells in a sample, by treating cells in the sample to
CC fix cellular contents, contacting fixed cells with the primer/probe which
CC is labelled with a radiolabel, a reporter group or a hapten, under
CC conditions which allow the probe to hybridize with 16S rRNA within the
CC fixed cell, removing unhybridized probe from the fixed cells, and
CC detecting the labeled probe-RNA hybrid by fluorescence in situ
CC hybridization. The primer/probe sequences are useful for identifying PAOs
CC that are capable of biologically removing phosphorus from waste water.
CC Rapid assessment of the presence of a number of PAOs in a waste water
CC sample, can be done using the primer/probe sequences. They allow quick
CC and convenient assessment of whether a sludge or waste water sample
CC includes PAOs and allows quantitation of PAO cells in samples

XX Sequence 1460 BP; 366 A; 338 C; 471 G; 283 T; 0 U; 2 Other;

Query Match 80.6%; Score 1160.6; DB 4; Length 1460;
Best Local Similarity 89.0%; Pred. No. 0;
Matches 1263; Conservative 1; Mismatches 153; Indels 2; Gaps 1;

Qy 24 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACCGGTAAACAGGGTGTTCGACC 83

Db 1 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACCGGCACGGGCAATCCT 60

Qy 84 GCTGACGAGTGGCGAACGGGTGAGTAATGCTCGGAATGTACCGTGTAAATGGGGGATAGC 143

Db 61 GGTGGCGAGTGGCGAACGGGTGAGTAATGATCGAATCGGAACGTCGCCCTGAAGTGGGGATAAC 120

Qy 144 TCGGCGAAAGCCGATTAAATACCGCATACGCCCTGAGGGGAAAGCGGGGATCGAAAGA 203
Db 121 GTAGCGAAGATTACGCTAATACCGCATATTCTGTGAGCAGGAAGAGGGGATCGCAAGA 180
Qy 204 CTTGCGGTTTATACAGCAGCCGACGTCGTGATTAGTATTGGTGGTGAAGAGTCAACCA 263
Db 181 CTTGCGCTTTGGGAGCGCGCATGTCGATTAGTATTGGTGGGCTAAAGGCTACCA 240
Qy 264 AGGGACGATCAGTAGCGGGTCTGAGNAGATGATCCGCCACACTGGGACTGAGACAGGC 323
Db 241 AGGCCAGATCCGTVAGCGGTCTGAGAGGATGATCCGCCACACTGGGACTGAGACAGGC 300
Qy 324 CCAGACTCTTACGGGAGCGCAGTAGTGGGGAATTTGGACAAATGGGGGCAACCCCTGATCCA 383
Db 301 CCAGACTCTTACGGGAGCGCAGTAGTGGGGAATTTGGACAAATGGGCGAAGCCCTGATCCA 360
Qy 384 GCATGCGCGTGTCTGAAGAAAGCCCTTCGGGTTGTAAGAGACTTTTGTGAGGAGGAAA 443
Db 361 GCCATGCCGCTGAGTGAAGAAAGCCCTTCGGGTTGTAAGAGCTCTTTCGGGGGGAAGAAA 420
Qy 444 TCCGCTGGTTAATACCGCGGGGATGACAGTACCBGAGAGATAAGCACCGGCTAACTA 503
Db 421 TTGCTCAGGATAATACCTCGAGTAGTAGCGGTACCCGAAAGAAAGACACCGGCTAACTA 480
Qy 504 CGTGCCAGCAGCCGCGTAATACGTAGGGTGCAAGCGTTAATCGGAATTACTGGCGCTAA 563
Db 481 CGTGCCAGCAGCCGCGTAATACGTAGGGTGCGAGCGTTAATCGGAATTACTGGCGCTAA 540
Qy 564 AGCGTGGCAGCGGCTTTTGCAGTCTGATGTGAAGCCCGGGCTCAACTGCGGAACGG 623
Db 541 AGCGTGGCAGCGGCTTTGTAAGACAGACGCTGAATCCCGGGCTCAACTGCGGAACGTG 600
Qy 624 CATTGGAGACTGCAAGACTAGAGTGGTTCAGAGGGGGGTAGAATTCCGCTGTAGCAGTG 683
Db 601 CGTTTGTGACTGCACGACTAGAGTGGCAGAGGGGGGTGGAATTCACGCTGTAGCAGTG 660
Qy 684 AAATGCGTAGAGATGCGGAGGAATACCGATGGCGAAGCAGCCCTCGGATGATCACCTGA 743
Db 661 AAATGCGTAGAGATGCGGAGGAACCGATGGCGAAGCAGCCCTCGGATGATCACCTGA 720
Qy 744 CGCTCATGCAAGAAAGCGTGGGAGCAACAGGATTAGATACCTGTGTAGTCCACGCCCT 803
Db 721 CGCTCATGCAAGAAAGCGTGGGAGCAACAGGATTAGATACCTGTGTAGTCCACGCCCT 780
Qy 804 AAACGATGCAATAGCTGTTG--GGGTTTGAATCCTTGGTAGCTAGCTAGCAGCTGA 861
Db 781 AAACGATGCAATAGCTGTTGTTGGGGTTAAACCCCATTTAGTCCGCTAACGCGTGA 840
Qy 862 AATTGACCGCTGGGAGTAGCGCCGCAAGGTTAAAACTCAAAGGAATTCGACGGGAGCCC 921
Db 841 AGTTGACCGCTGGGAGTAGCGCCGCAAGGTTAAAACTCAAAGGAATTCGACGGGAGCCC 900
Qy 922 GCACAGCGGTGATGATGGAATTAATTCGATGCAACGCAAAAAACCTTACCTGCTCTT 981
Db 901 GCACAGCGGTGATGATGGAATTAATTCGATGCAACGCAAAAAACCTTACCTGCTCTT 960
Qy 982 GACATGTACGGAATTTGGTAGAGATATCTTGGTGGCCGAAAGGGAGCGGTAAACACAGTG 1041
Db 961 GACATGTACGGAATTCCTGAAGAGATTTCGGGAGTGGCCGAAAGGGAGCGCTGAACACAGTG 1020
Qy 1042 CTCATGGCTGTCGTGAGCTCGTGTGCTGAGATGTTGGGTAAAGTCCCGCAACGAGGCGCA 1101
Db 1021 CTCATGGCTGTCGTGAGCTCGTGTGCTGAGATGTTGGGTAAAGTCCCGCAACGAGGCGCA 1080
Qy 1102 ACCCTTGTCTATTAGTTGCCATCAATTTAGTTGGGCACTCTAATGAGACTGCGGCTGACAA 1161
Db 1081 ACCCTTGTCTAATTTAGTTGCCATCAATTTAGTTGGGCACTCTAATGAAACCTGCGGCTGACAA 1140
Qy 1162 CCGGAGGAGGTGGGATGACGTCAAGTCTCTATGSCCTTATGAGCAGCGGCTTCACAGC 1221
Db 1141 CCGGAGGAGGTGGGATGACGTCAAGTCTCTATGSCCTTATGAGGAGGCTTCACAGC 1200

QY 1222 TCATACAAATGTCGTACAGAGGTCGTAAAGCCGAGGTGGTGCCTCAATCTCATAAAC 1281
DDB 1201 TCATACAAATGTCGTACAGAGGTTGCCAAGCCGAGGTGGAGCCCAATCACAGAAGC 1260
QY 1282 CGATCGTAGTCCGATCGCACTCTGCAACTCGAGTCGCTGAAGTCGGAATCGCTAGTAAT 1341
DDB 1261 CGATCGTAGTCCGATTCGAGTCTGCAACTCGACTGCAATGAAGTCGGAATCGCTNGTAAT 1320
QY 1342 GCGAGATCAGATGTCGGGTGAATACGTTCCCGGTCTTGTACACACCGCCCTCACAC 1401
DDB 1321 GCGGATCAGCATGTCGCGGTGAATACGTTCCCGGTCTTGTACACACCGCCCTCACAC 1380
QY 1402 CATGGAGTGAAGTTTACCCAGAAGTCGGTGAAGCTAAACG 1440
DDB 1381 CATGGAGCGGGTCTGCCAGAAGTAGTTAGCCTTAACCG 1419

RESULT 7
ADB61690
ID ADB61690 standard; DNA; 1488 BP.
XX
AC ADB61690;
XX
DT 04-DEC-2003 (first entry)
XX
DE 16S rRNA of Burkholderia mallei DNA sequence.
XX
KW enriching mRNA; high quality bacterial mRNA; bacterial gene expression;
KW poly-A tail; mRNA purification; oligo-dT capture;
KW prokaryote mRNA purification; bridging oligonucleotide; targeting region;
KW capture oligonucleotide; prokaryotic 16S rRNA; prokaryotic 23S rRNA;
KW eukaryotic 17S rRNA; eukaryotic 18S rRNA; eukaryotic 28S rRNA;
KW 28S eukaryotic rRNA bridging oligonucleotide; ds.
XX
OS Burkholderia mallei.
XX
PN WO2003054162-A2.
XX
PD 03-JUL-2003.
XX
PF 19-DEC-2002; 2002WO-US041014.
XX
PR 20-DEC-2001; 2001US-00029397.
XX
PA (AMBI-) AMBION INC.
XX
PI Murphy GL, Whitley JP;
XX
XX WPI; 2003-663255/62.
XX
PT Depleting or isolating targeted nucleic acids e.g. rRNA, involves using a
PT bridging oligonucleotide comprising bridging region and a targeting
PT region complementary to a targeted nucleic acid, and a capture
PT oligonucleotide.
XX
PS Claim 4; Page 174; 208pp; English.
XX
XX This invention relates to a novel method for isolating, depleting or
CC separating a targeted nucleic acid, such as rRNA, from a sample
CC comprising targeted and non-targeted nucleic acids. It effects a way of
CC enriching for non-targeted nucleic acids such as mRNAs. Isolating
CC sufficient quantities of high quality bacterial mRNA is a demanding
CC process which impedes analysis of bacterial gene expression in the
CC presence of host cells. A small percentage of bacterial mRNAs may be poly
CC -A tailed, but these are targeted for degradation and tend to be
CC unstable. As a result, the commonly employed method for mRNA purification
CC with eukaryotic cells, oligo-dT capture, is ineffective. The present
CC invention provides an alternative, more suitable method for mRNA
CC purification from prokaryotes. The method of the invention comprises the
CC incubation of a sample with a bridging oligonucleotide (containing a
CC targeting region) and subsequently incubating with a capture
CC oligonucleotide allowing the isolation of the target from the sample. The
CC method is useful for depleting or isolating targeted nucleic acid, for

CC example rRNA such as prokaryotic 16S or prokaryotic 23S, eukaryotic 17S
CC or 18S or eukaryotic 28S rRNA, from a sample. The rRNA sequence may
CC comprise any one of 64 fully defined sequences as given in the
CC specification. The present sequence is that of a DNA sequence which
CC represents the sequence of 16S rRNA of Burkholderia mallei related to the
CC invention.
XX
SQ Sequence 1488 BP; 373 A; 344 C; 480 G; 291 T; 0 U; 0 Other;
Query Match 80.68; Score 1159.8; DB 10; Length 1488;
Best Local Similarity 89.14; Pred. No. 0;
Matches 1264; Conservative 1; Mismatches 149; Indels 5; Gaps 1;
QY 22 AGATTGAACGCTGGCGCATGCTTTACACATGCAAGTCGAACGGTAACAGGGTCTTGCA 81
DDB 1 AGATTGAACGCTGGCGCATGCTTTACACATGCAAGTCGAACGGCAGCACGGGCTTCGC 60
QY 82 CCGCTGACGAGTGGCGAACCGGTGAGTAATTCGCTCGGAATGTACCGTGTAAATGGGGATA 141
DDB 61 CTGGTGGCGAGTGGTGAACGGGTGAGTAATACATCGGAACATGTCTGTGTAGTGGGGATA 120
QY 142 GCTCGGCGAAAGCCGGAATTAATACCGCATACGCTCTGAGGATGAAGCGGGGATCGAA 201
DDB 121 GCCCGCGAAAGCCGGAATTAATACCGCATACGCTCTGAGGATGAAGCGGGGACCTTCG 180
QY 202 GACCTCGCTTTATACGAGCAGCCGACGTCTGATTAGTGTAGTGAAGTAAAGAGCTCAC 261
DDB 181 GGCTTCGCGCTATAGGTTGGCGATGGCTGATTAGTGTGGTGGGTAAAGCCTTAC 240
QY 262 CAAGCGCAGCATAGTACGCGGTCTGAGAGATGATCCGCCACACTGGGACTGAGACAG 321
DDB 241 CAAGCGCAGCATAGTACGCTGCTGAGAGACACACGACGACGACGACGACGACGACG 300
QY 322 GCCCAGACTCTACGCGAGCAGCAGTGGGGAATTTGGCAATGGGGGCAACCTGTATC 381
DDB 301 GCCCAGACTCTCTACGCGAGCAGCAGTGGGGAATTTGGCAATGGGGGCAACCTGTATC 360
QY 382 CAGCCATGCGCGCTGCTGAAGAAAGGCTTCGCGGTGTGAAGGACTTTTGTTCAGGAGGA 441
DDB 361 CAGCAATGCCCGCTGTGTGAAGAGGCTTCGCGGTGTGAAGCACTTTTGTTCGGAAGA 420
QY 442 AATCCCGCTGTTAATACCCCGCGGGATGACAGTACCBGAAGAATAAGCACCGGCTAAC 501
DDB 421 AATCAATTCGGCTAATACCCCGAGTGGATGACGCTACCGGAAGAATAAGCACCGGCTAAC 480
QY 502 TAGTGCAGCAGCGCGGTAAATAGTAGGTGCAAGCTTAATCGGAATTAATCTGGGCGT 561
DDB 481 TACGTGCAGCAGCGCGGTAAATAGTAGGTGCAAGCTTAATCTGGGCGT 540
QY 562 AAAGCTGCGCAGCGGTTTTGCAAGTCTGATGTGAAGCCCGGGCTCAACCTGGGGAAC 621
DDB 541 AAAGCTGCGCAGCGGTTTTGCAAGCTGATGTGAATCCCGGGCTCAACCTGGGGAAC 600
QY 622 GGCATTGGAGACTGCAAGACTAGTAGTCGTGAGAGGGGGTAGAATTCGCGGTGTAGCAG 681
DDB 601 TGCAATGGTACTGCGCAGGCTAGAGTATGGCAGAGGGGGTAGAATTCACGCTGTAGCAG 660
QY 682 TGAATGCTGAGATGCGGAGGAATACCGATGCGGAGGAGCGCCCTCGGATGACACT 741
DDB 661 TGAATGCTGAGATGCGGAGGAATACCGATGCGGAGGAGCGCCCTCGGATGACACT 720
QY 742 GACGCTCATGCAAGAAAGCGTGGGAGCAAAACAGGATTAGATACCTCGGTAGTCCACGCC 801
DDB 721 GACGCTCATGCAAGAAAGCGTGGGAGCAAAACAGGATTAGATACCTCGGTAGTCCACGCC 780
QY 802 CTAACAGATGTCATTAAGTCTGTGGGGTTTGAATCTCTTGGTAGGTAGCTTAACCGCTGA 861
DDB 781 CTAACAGATGTCATTAAGTCTGTGGGGTTTGAATCTCTTGGTAGGTAGCTTAACCGCTGA 840
QY 862 AATTGACCGCTGGGAGTACGCGCGCAAGGTGTAACCTCAAGGAATTTGACGGGACCC 921
DDB 841 AGTTGACCGCTGGGAGTACGCGCGCAAGGTGTAACCTCAAGGAATTTGACGGGACCC 900

Qy	478	CBGNAAGNATTAAGCACCGGCTAACTACGTGCACGACGCCGCGGTAAATACGTAGGGTGCAA	537
Db	489	CCTGAAGAATTAAGCACCGGCTAACTACGTGCACGACGCCGCGGTAAATACGTAGGGTGCGA	548
Qy	538	CGGTTAATTCGGAATTACTTGGCGCGTAAAGCGTGCAGCGCGGTTTTCGAAGTCTCATGTGGA	597
Db	549	CGGTTAATTCGGAATTACTTGGCGCGTAAAGCGGCGCAGACGGTTACTTAAGCAGCATGTGA	608
Qy	598	AAGCCCGGGCTCAACCTGGGAAACGGCAATTGAGACTGCAAGACTAGAGTCGCTCAGAGG	657
Db	609	AATCCCGGGCTCAACCCGGGAACCTGCGTTCTGAACCTGGGTGACTCGAGTGTGTTCAGAGG	668
Qy	658	GGGCTAGAAATTCGCGTGTACAGTGAATCGGTAGAGATCCGAGAGGAATAACCGATGGCG	717
Db	669	GAGGTAGNAATTCACGCTGTACAGTGAATTCGCTAGAGATGTGGAGGAAATACCGATGGCG	728
Qy	718	AAGCAGCCCCCTGGGATGACACTGACGCTCATGCAAGAAAGCTGGGGAGCAACACAGGA	777
Db	729	AAGCAGCCTCTTGGGACAAACACTGAACGTTATGCCGAAAGCGTGGGTAGCAACACAGGA	788
Qy	778	TTAGATACCCCTGGTGTAGTCCAGCCCTAAACCGATGTCATATTAGCTGTTGGG--GGTTTCGAT	836
Db	789	TTAGATACCCCTGGTGTAGTCCAGCCCTAAACCGATGTCATATTAGCTGTTGGGCAACCTGATT	848
Qy	837	CTTTGGTAGCGTAGCTAAACGCGTGAATTTGACCCGCTGGGAGTACGCGCGCAAGGTTAA	896
Db	849	GTTTGGTAGCGTAGCTAAACGCGTGAATTTGACCCGCTGGGAGTACGCTCGCAAGATTAA	908
Qy	897	AACCTCAAGGAATTTGACGGGACCCGCACACGCGTGGATGATGTGATTAATTCGATGC	956
Db	909	AACCTCAAGGAATTTGACGGGACCCGCACACGCGTGGATGATGTGATTAATTCGATGC	968
Qy	957	AACCGCAAAACCTTACTCGTCTCTTGACATGTACCGAACTTGGTAGAGATATCTTGTGTC	1016
Db	969	AACCGGAAGAACCTTACTCGTCTTGACATGTACCGAA--TCCTCCGGAGACGAGAGT	1026
Qy	1017	CCGAACGGGAGCCGTAAACACAGGTGCTGCATGGCTGTGTCGTCAGCTCGTGTGAGATGT	1076
Db	1027	GCCTTCGGGAGCCGTAAACACAGGTGCTGCATGGCTGTGTCGTCAGCTCGTGTGAGATGT	1086
Qy	1077	TGGGTTAAGTCCCGCAACGAGCGCAACCTTGTCAATTAGTTGCCATCATTTAGTTGGGCA	1136
Db	1087	TGGGTTAAGTCCCGCAACGAGCGCAACCTTGTCAATTAGTTGCCATCATTTAGTTGGGCA	1146
Qy	1137	CTCTAATGAGATGCCGGTGAACAAACCGAGGAAGGTGGGATGACGTCAAGTCCCTCATG	1196
Db	1147	CTCTAATGAGATGCCGGTGAACAAACCGAGGAAGGTGGGATGACGTCAAGTCCCTCATG	1206
Qy	1197	GCCCTTATGACAGGGCTTACACGTCTACAAATGGTCCGTACAGAGGGTCGTAAACCG	1256
Db	1207	GCCCTTATGACAGGGCTTACACGTCTACAAATGGTCCGTACAGAGGGTAGCCACGCCG	1266
Qy	1257	CGAGGTGGTGCAAATCTCATAAACCGATCGTAGTCGGATCGCACTCTCGCAACTCGAGT	1316
Db	1267	CGAGGCGGAGCCAATCTCACAAACCGATCGTAGTCGGATTCGCACTCTCGCAACTCGAGT	1326
Qy	1317	CGGTGAAGTCGGAAATCGTGTAGTAATTCGAGATCAGCATGTCTGGGTGAATACGTTCCCGG	1376
Db	1327	GCATGAAGTCGGAAATCGTGTAGTAATTCGAGGTTCAGCATCTCGCGGTGAATACGTTCCCGG	1386
Qy	1377	GTCCTGTGTACACCGCCCGCTCACACCATGGGAGTGAGTTTACCAGAAAGTGGGTAGGCTA	1436
Db	1387	GTCTTGTGTACACCGCCCGCTCACACCATGGGAGTGGGGATACCAAGGTAGGTAGGNTA	1446
Qy	1437	ACC	1439
Db	1447	ACC	1449

RESULT 10

AAA81490 00

WP Sequence split into 15 fragments LOCUS AAA81490 Accession Aaa81490

WP	Fragment Name	Begin	End
WP	AAA81490_00	1	110000
WP	AAA81490_01	100001	210000
WP	AAA81490_02	200001	310000
WP	AAA81490_03	300001	410000
WP	AAA81490_04	400001	510000
WP	AAA81490_05	500001	610000
WP	AAA81490_06	600001	710000
WP	AAA81490_07	700001	810000
WP	AAA81490_08	800001	910000
WP	AAA81490_09	900001	1010000
WP	AAA81490_10	1000001	1110000
WP	AAA81490_11	1100001	1210000
WP	AAA81490_12	1200001	1310000
WP	AAA81490_13	1300001	1410000
WP	AAA81490_14	1400001	1437668
ID	AAA81490 standard; DNA; 1437668 BP.		
XX	AAA81490;		
AC			
XX	04-DEC-2000 (first entry)		
DT			
XX			
DE	N. meningitidis B full length genome DNA sequence SEQ ID NO:1068.		
XX			
KW	Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;		
KW	antigen; vaccine; diagnosis; infection; antibacterial; identification;		
KW	Meningococcus B; MenB; ds.		
XX			
OS	Neisseria meningitidis.		
XX			
PN	WO200022430-A2.		
XX			
PD	20-APR-2000.		
XX			
XX	08-OCT-1999; 99WO-US023573.		
PF			
XX			
PR	09-OCT-1998; 98US-0103794P.		
PR	30-APR-1999; 99US-0132068P.		
XX			
PA	(CHIR) CHIRON CORP.		
XX			
FI	Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;		
PI	Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;		
PI	Rappuoli R, Pizza M;		
XX			
DR	WPI; 2000-318079/27.		
XX			
PT	Isolated nucleotide sequences of Neisseria meningitidis which can be used		
PT	in the diagnosis and treatment of N. meningitidis infection and other		
PT	Neisserial infections, for example, N.gonorrhoea.		
XX			
PS	Claim 7; Page 866-1272; 1760pp; English.		
XX			
CC	The present invention describes methods of obtaining immunogenic proteins		
CC	from Neisseria genomic sequences. AAA81453 to AAA82414 represent		
CC	specifically claimed Neisseria meningitidis genomic DNA sequences;		
CC	AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA		
CC	sequences and their corresponding proteins; AAA81254 to AAA81259 and		
CC	AAA81304 to AAA81321 represent PCR primers used in the isolation of		
CC	Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent		
CC	Neisseria meningitidis MenB polynucleotide ORF sequences, which are all		
CC	used in the exemplification of the present invention. The nucleic acid		
CC	sequences, protein sequences, and antibodies against them, can be used in		
CC	the manufacture of a composition. The composition can be used as a		
CC	medicament (or in the manufacture of a medicament) for treating,		
CC	preventing or diagnosing infection due to Neisserial bacteria. For		
CC	example, some of the identified proteins could be components of vaccines		
CC	against Meningococcus B; against all serotypes; and/or against all		
CC	pathogenic Neisariae. Identification of sequences from the bacterium		
CC	will also facilitate production of biological probes, particularly		
CC	organism-specific probes. Attempts to make efficacious Meningococcus B		
CC	vaccines have failed mainly due to antigen tolerance. Multivalent		
CC	vaccines have also been tried but none have successfully overcome		

CC antigenic variability. The provision of further, complete sequences may
CC provide an opportunity to identify secreted or surface exposed proteins
CC that may be presumed targets for the immune system and which are not
CC antigenically variable or at least more conserved than other more
CC variable regions

AA	Sequence	1437668 BP; 344338A; 353206C; 395074G; 355045T; 0U; 50ther;
SQ	Query Match	80.5%; Score 1159; DB 3; Length 110000;
	Best Local Similarity	89.1%; Pred. No. 0;
	Matches 1286; Conservative	1; Mismatches 147; Indels 9; Gaps 3;
Qy	4	AGAGTTTGATCCTGGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAC 63
Db	60972	AGAGTTTGATCCTGGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAC 61031
Qy	64	GGTA-----ACAGGTGCTTGCAACGCTGACAGATGGCGAAACGGGTGAGTAATCGTCG 117
Db	61032	GGCAGCACAGAGAAGCTTGCTTCTCGGGTGGCGATGGCGAAGGGTGAGTAACATATCG 61091
Qy	118	GAATGTACTCGTTAAATGGGGGATAGCTCGGCGGAAGCCGGAATTATACGCNATAGCCCT 177
Db	61092	GAACGTACCGAGTAGTGGGGGATAACTGATCGAAAGATCAGCTAATACCGCATAGCTTT 61151
Qy	178	GAGGGGAAGCGGGGATCGAAGACCTTCGGTATTACGACGCCGACGCTCTGATTAG 237
Db	61152	GAGAGAAAGCAGGGGACCTTCGGGCTTGGCGCTATTCCGCGCGCGGATATCTGATTAG 61211
Qy	238	CTAGTTCGTGAGGTAAAGAGCTCACCAAGGCGACGATCAGTAGCGGTCTTGAGAGGATGAT 297
Db	61212	CTAGTTCGTGGGTAAAGGCTTACCAAGGCGACGATCAGTAGCGGTCTTGAGAGGATGAT 61271
Qy	298	CCGCCACACTGGGACTGAGACACGGGCCAGATCTTACGGGAGGACAGTAGTGGGAAATTT 357
Db	61272	CCGCCACACTGGGACTGAGACACGGGCCAGACTCTTACGGGAGGACAGTAGTGGGAAATTT 61331
Qy	358	TGGCAATGGGGCAACCTGATCCAGCCATGCGCGTGTCTGAGAAGGCCCTTCGGTT 417
Db	61332	TGGCAATGGGCGCAACCTGATCCAGCCATGCGCGTGTCTGAGAAGGCCCTTCGGTT 61391
Qy	418	GTAAGGACTTTTGTTCAGGGAGGAAATCCCGCTGGTTAATACCCGGCGGGGATGACAGTA 477
Db	61392	GTAAGGACTTTTGTTCAGGGAGGAAAGGCTGTGCTAATATCAGCGGCTGATGACGGTA 61451
Qy	478	CCBGAAGAATAAGCACCGGTAACTAGTCCAGCAGCCGCGGTAACTAGTAGGTGCA 537
Db	61452	CCTGAAGAATAAGCACCGGTAACTAGTCCAGCAGCCGCGGTAACTAGTAGGTGCGA 61511
Qy	538	CGCTTAATCGGAATTACTGGCGGTAAAGCTGCGCAGGCGGTTTTCAGAGTCTGATGTGA 597
Db	61512	CGCTTAATCGGAATTACTGGCGGTAAAGCGGGCGCAGACGGTTACTTAAGCAGGATGTA 61571
Qy	598	AAGCCCGGGCTCAACCTGGGAACGGCAITGGAGACTGCAAGACTAGTGCCTCAGAGG 657
Db	61572	AATCCCGGGCTCAACCCGGGAACCTGGTTCTGAACTGGGTGACTCGAGTGTCCAGAGG 61631
Qy	658	GGGTAGAAATTCGCCGTGTAGCAGTGAATCGGTAGAGATCGGAGGAATACCGATGGG 717
Db	61632	GAGGTAGAAATTCACCGTGTAGCAGTGAATGCCGTAGAGATGTGGAGGAATACCGATGGG 61691
Qy	718	AAGCAGGCCCTCGGATGACACTGACGCTCATGCGACAGAAAGCGTGGGAGCAAAACAGA 777
Db	61692	AAGCAGGCTCTCTGGGACACACTGACGTTTATGCCGGAAGCGTGGTAGCAACACAGA 61751
Qy	778	TTAGATACCTTGGTAGTCCAGCCCTAAAAGATGTCAATTAGCTGTGTGGG-GGTTGAAT 836
Db	61752	TTAGATACCTTGGTAGTCCAGCCCTAAAAGATGTCAATTAGCTGTGTGGGCAACCTGAT 61811
Qy	837	CTTGTGTAGCTAGCTAACGGTGAATTCACCGCTGGGAGTACGGCGCAAGGTTAA 896
Db	61812	GCTTGGTAGCTAGCTAACGGTGAATTCACCGCTGGGAGTACGGTCCGAAGATTAA 61871
Qy	897	AACTCAAAAGGAATTCAGGGGACCCGACCAAGCGGTGGATGTGTGATTAATTCCATGTC 956

QY 118 GAATGTACCGTCTTAATGGGGGATAGCTCGCGAAGCCGCGATTAAATACCCATACGCCCT 177
Db 107842 GAACTGACCGAGTAGTGGGGATAACTGATCGAAAGATACGCTAAATACCGCATACGCTTT 107901
QY 178 GAGGGGAAAGCCGGGATCGAAAGACCTCGCGTTATACAGAGCCGAGCTCTGATTAG 237
Db 107902 GAGAGAAAGCAGGGGACCTTCGGGCTTCGCGTATTCAGAGCGCGGATATCTGATTAG 107961
QY 238 CTAGTTGGTGAAGTAAGAGCTCACAAAGGGGACGATCAGTAGCGGGTCTGAGAGGATGAT 297
Db 107962 CTAGTTGGTGAAGGGCTTACCAAGGGGACGATCAGTAGCGGGTCTGAGAGGATGAT 108021
QY 298 CCGCCACACTCGGGACTGAGACACCGGCCAGACTCCTACGGGAGGACGACGATGGGGAATTT 357
Db 108022 CCGCCACACTCGGGACTGAGACACCGGCCAGACTCCTACGGGAGGACGACGATGGGGAATTT 108081
QY 358 TGGACATGGGGCAACCTGATCCAGCGATGCCGCTGCTCGAAGAGCCCTTCGGGTT 417
Db 108082 TGGACATGGGGCAAGCCCTGATCCAGCGATGCCGCTGCTCGAAGAGCCCTTCGGGTT 108141
QY 418 GTAAAGGACTTTTGTCAAGGAGGAATCCCGCTGGTTAAATACCCGCGGGGATCACAGTA 477
Db 108142 GTAAAGGACTTTTGTCAAGGAGGAATCCCGCTGGTTAAATACCCGCGGGGATCACAGTA 108201
QY 478 CCBGAAGAATAAGCACCGGCTTAACCTGCGAGCAGCCGGGTAACTACGTAGGGTGCAA 537
Db 108202 CCTGAAGAATAAGCACCGGCTTAACCTGCGAGCAGCCGGGTAACTACGTAGGGTGCAA 108261
QY 538 GCGTTAATCGGAATTAAGCTGGCGTAAAGCGTGGCAGCGGTTTGAAGTCTGATGTA 597
Db 108262 GCGTTAATCGGAATTAAGCTGGCGTAAAGCGTGGCAGCGGTTTGAAGTCTGATGTA 108321
QY 598 AAGCCCGGGCTCAACCTGGGAAACCGGCTTGGAGACTGCAAGACTAGAGTGGCTCAGAGG 657
Db 108322 AATCCCGGGCTCAACCGGGAACTGGCTTCTGNACTGGGTGACTCAGTGTGTGAGG 108381
QY 658 GGGGTAGAAATCCCGGTGTAGAGTGAATTCGCTAGAGATGCGGAGGAATACCGATGGCG 717
Db 108382 GAGGTAGAAATTCACGCTGTAGCAGTGAATTCGCTAGAGATGTCGAGGAATACCGATGGCG 108441
QY 718 AAGCAGCCCTCGGGATGACACTGACGCTCATGCAAGAGCGTGGGAGCAACAGGA 777
Db 108442 AAGCAGCCCTCGGGATGACACTGACGCTCATGCAAGAGCGTGGGATGCAACAGGA 108501
QY 778 TTAGATACCTCGTAGTCCACGCGCTTAAACGATGTCAATTAGCTGTGGG-GGTTTGAAT 836
Db 108502 TTAGATACCTCGTAGTCCACGCGCTTAAACGATGTCAATTAGCTGTGGCAACCTGAT 108561
QY 837 CCTTGGTAGCGTAAACCGGTGAATTCACCGCTTGGGAGTACGGCCGCAAGGTAA 896
Db 108562 GCTTGGTAGCGTAAACCGGTGAATTCACCGCTTGGGAGTACGGTCGCAAGATTAA 108621
QY 897 AACTCAAGGAATGAGGGGACCCGACAAAGCGGTGGATGATGTGGATTAATTCGATGC 956
Db 108622 AACTCAAGGAATGAGGGGACCCGACAAAGCGGTGGATGATGTGGATTAATTCGATGC 108681
QY 957 AACCGAAAAACCTTACTGCTCTTGACATGTACGGAACTTGGTAGAGATATCTTGGTGC 1016
Db 108682 AACCGAAAAACCTTACTGCTCTTGACATGTACGGAACTTGGTAGAGATATCTTGGTGC 108739
QY 1017 CCGAAAGGGAGCGGTAAACAGAGTGTGCAATGCTGTCGTCAGCTCGTGTGTCGATGAT 1076
Db 108740 GCTTTCGGGAGCGGTAAACAGAGTGTGCAATGCTGTCGTCAGCTCGTGTGTCGATGAT 108799
QY 1077 TGGTTTAAGTCCCGACAGAGCCCAACCTTGTTCATTTAGTTGGCATCATTTAGTTGGCA 1136
Db 108800 TGGTTTAAGTCCCGACAGAGCCCAACCTTGTTCATTTAGTTGGCATCATTTAGTTGGCA 108859
QY 1137 CTCTAATGAGACTGCGGTCACAAAACCGGAGGAAGTGGGGATGACGTCAAGTCTTCATG 1196
Db 108860 CTCTAATGAGACTGCGGTCACAAAACCGGAGGAAGTGGGGATGACGTCAAGTCTTCATG 108919
QY 1197 GCCCTTATGAGCAGGGCTTCCACGCTCATCAATGTGTGCTACAGAGGGTTCGTAAGCCG 1256

Db 108920 GCCCTTATGACCAAGGCTTCACACGTCATCAATGGTTCGGTACAGAGGTAGCAAGCCG 108979
QY 1257 CGAGGTGGTCCCAATCTCATAAACCGATCGTAGTCCGATCCACTCTGCAACTCGAGT 1316
Db 108980 CGAGGCGGAGCCAATCTCAAAACCGATCGTAGTCCGATTCGACTCTGCAACTCGAGT 109039
QY 1317 GCCTGAAGTCGGAATCGTAGTAAATCGCAGATCAGCATGCTCGGCTGAAATACGTTCCCG 1376
Db 109040 GCATGAAGTCGGAATCGTAGTAAATCGCAGGTGAGCATCTGCGGTGAATACGTTCCCG 109099
QY 1377 GTCTTGTACACACCGCCGCTCACCATGAGGATGAGTTTTCACAGAGTGGGTAGGCTA 1436
Db 109100 GTCTTGTACACACCGCCGCTCACCATGAGGATGAGTTTTCACAGAGTGGGTAGGATA 109159
QY 1437 ACC 1439
Db 109160 ACC 109162

RESULT 12

AAA81490_03

Continuation (4 of 15) of AAA81490 from base 300001 (N. meningitidis B full length genome
WP Sequence split into 15 fragments LOCUS AAA81490 Accession AAA81490

WP	Fragment Name	Begin	End
WP	AAA81490_00	1	110000
WP	AAA81490_01	100001	210000
WP	AAA81490_02	200001	310000
WP	AAA81490_03	300001	410000
WP	AAA81490_04	400001	510000
WP	AAA81490_05	500001	610000
WP	AAA81490_06	600001	710000
WP	AAA81490_07	700001	810000
WP	AAA81490_08	800001	910000
WP	AAA81490_09	900001	1010000
WP	AAA81490_10	1000001	1110000
WP	AAA81490_11	1100001	1210000
WP	AAA81490_12	1200001	1310000
WP	AAA81490_13	1300001	1410000
WP	AAA81490_14	1400001	1437668

Query Match 80.5%; Score 1159; DB 3; Length 110000;

Best Local Similarity 89.1%; Pred. No. 0;

Matches 1286; Conservative 1; Mismatches 147; Indels 9; Gaps 3;

QY 4 AGAGTTTGCCTCGCTCAGATTGAACGCTGGCGCATGCTTTACACATCGAAGTCGAAC 63
Db 7722 AGAGTTTGCCTCGCTCAGATTGAACGCTGGCGCATGCTTTACACATCGAAGTCGAAC 7781
QY 64 GGTA-----ACAGGGTGTCTGCACCGCTGACGAGTGGCGAAACGGGTGAGTAATGCGTCG 117
Db 7782 GGCAGCACAGAGAGCTTCTTCTCGGTGGCGAGTGGCGAACGGGTGAGTAACATATCG 7841
QY 118 GAATGTACCGTGAATGGGGATAGCTCGCGCGAAGCCGAGTTAATACCGCATACGCCCT 177
Db 7842 GAACGTACCGAGTAGTGGGGATTAAGTATCGAAGATCAGCTAATACCGCATACGCTTT 7901
QY 178 GAGGGGAAAGCGGGGATCGAAGACCTCGGTTATACGAGCAGCGGCTGATTAG 237
Db 7902 GAGAGAGAAGCAGGGGACCTTCGGGCCCTTCGCGCTATTTCGAGCGCGCATATCTGATTAG 7961
QY 238 CTAGTTGGTGAAGTGAAGCTCACCAAGGCGACGATCAGTAGCGGCTCTGAGAGGATGAT 297
Db 7962 CTAGTTGGTGGGTAAAGGCTTACCAGGCGACGATCAGTAGCGGCTCTGAGAGGATGAT 8021
QY 298 CCGCCACACTCGGAGTGAACACCGGCCAGACTCTTACCGGAGGACGAGTGGGGAAATTT 357
Db 8022 CCGCCACACTCGGAGTGAACACCGGCCAGACTCTTACCGGAGGACGAGTGGGGAAATTT 8081
QY 358 TGGACATGGGGCAACCTTGCATCCAGCCATGCCGCTGCTCTGAAGAGCCCTTCGGGTT 417
Db 8082 TGGACATGGGGCAACCTTGCATCCAGCCATGCCGCTGCTCTGAAGAGCCCTTCGGGTT 8141

Qy 418 GTAAGGACCTTTCTCAGGGAGGAATCCCGCTGGTTAATACCCGCGGGGATGACAGTA 477
Db 8142 GTAAAGGACCTTTCTCAGGGAGGAATAAGCGCTGGTTAATATCATCGCGCTGATACCGGTA 8201
Qy 478 CCBGAAGAATAAGCACCGGCTAACTAGCTGCCAGCAGCCGCGTAATACGTAGGGTGCAA 537
Db 8202 CCTGAGNAATPAGCACCGGCTAACTAGCTGCCAGCAGCCGCGTAATACGTAGGGTGCGA 8261
Qy 538 GCCTTAATCGGAATTACTTGGCGTAAAGCGGTGCGAGCGCGTGGTAAAGTCTGATGTA 597
Db 8262 GCGTTAATCGGAATTACTTGGCGTAAAGCGGTGCGAGCGGTGGTAAAGTCTGATGTA 8321
Qy 598 AAGCCCCGGCTCAACTGGGAACGGCATTTGGAGACTGCAAGACTAGAGTCCGTCAGAG 657
Db 8322 AATCCCCGGCTCAACCGGGAACTGCGTTCTGAACCTGGGTGACTCGAGTGTGCAGAGG 8381
Qy 658 GGGGTAGAAATCCCGTGTAGCAGTGAATCCGTAGAGATCCGAGGAATAACCGATGGCG 717
Db 8382 GAGGTAGAAATCCAGGTGTAGCAGTGAATCCGTAGAGATGTGGAGNAATACCGATGGCG 8441
Qy 718 AAGCAGCCCCCTGGGATGACACTGACGCTCATGCAAGAAAGCGTGGGGACAAACAGGA 777
Db 8442 AAGCAGCCCTCCTGGGACAACTGACGTTTATGCTTCAATTTAGCTGTTGGGCAACCTGAT 8501
Qy 778 TTAGATACCCCTGGTAGTCCAGCCCTAAACGATGTCAATTTAGCTGTTGGGCAACCTGAT 836
Db 8502 TTAGATACCCCTGGTAGTCCAGCCCTAAACGATGTCAATTTAGCTGTTGGGCAACCTGAT 8561
Qy 837 CTTTGGTAGCTAGCTAAACCGGTGAATTTGACCGCTCGGGGAGTACGGCCCAAGGTTAA 896
Db 8562 CTTTGGTAGCTAGCTAAACCGGTGAATTTGACCGCTCGGGGAGTACCGTCCAGAGTTAA 8621
Qy 897 AACTCAAGGAATTAAGCGGACCGCAACAGCGGTGGATGATGTGGANTTAATTCGATGC 956
Db 8622 AACTCAAGGAATTAAGCGGACCGCAACAGCGGTGGATGATGTGGANTTAATTCGATGC 8681
Qy 957 AACGGGAACCTTACCTGCTTTGACATGTACGGAACCTTGGTAGAGATATCTTGGTGC 1016
Db 8682 AACGGGAACCTTACCTGCTTTGACATGTACGGAACCTTGGTAGAGATATCTTGGTGC 8739
Qy 1017 CCGAAAGGAGCGGTAAACACAGGTGCTGCATGGCTGCTCAGCTCGTGTGCTGAGATGT 1076
Db 8740 GCCTTCCGGAGCGGTAAACACAGGTGCTGCATGGCTGCTCAGCTCGTGTGCTGAGATGT 8799
Qy 1077 TGGGTTAAGTCCCGCAACGAGCGCAACCCCTTGTCAATTTAGTTGCCATCAATTTAGTTGGCA 1136
Db 8800 TGGGTTAAGTCCCGCAACGAGCGCAACCCCTTGTCAATTTAGTTGCCATCAATTTAGTTGGCA 8859
Qy 1137 CTCTAATGAGACTGCCGTGACAAACCGGAGGAGGTGGGATGACGTCAAGTCTCATG 1196
Db 8860 CTCTAATGAGACTGCCGTGACAAACCGGAGGAGGAGGTGGGATGACGTCAAGTCTCATG 8919
Qy 1197 GCCCTTATGAGCAGGCTTCAACGCTCATCAATGGTCCGTACAGAGGCTCGCTAAGCCG 1256
Db 8920 GCCCTTATGAGCAGGCTTCAACGCTCATCAATGGTCCGTACAGAGGCTCGCTAAGCCG 8979
Qy 1257 CGAGTGTGCAATCTCATAAACCGATCGTGTGCTGGATCGCACTCTGCAACCTCGAGT 1316
Db 8980 CGAGGCGGAGCCAACTCATCAAAACCGATCGTGTGCTGGATTTGCACTCTGCAACCTCGAGT 9039
Qy 1317 GCGTGAATCGGAATCGGTAGTAATCGGAGTACGATCGCTGCGGTGAATAGTTCCCGG 1376
Db 9040 GCATGAAGTCGGAATCGGTAGTAATCGGAGGTACGATACCTGCGGTGAATAGTTCCCGG 9099
Qy 1377 GTCTTGTACACACCGCCGCTCACACCATGGGAGTCAAGTTTCAACGAGAGTGGGTAGGCTA 1436
Db 9100 GTCTTGTACACACCGCCGCTCACACCATGGGAGTGGGAGTACGAGAGTGGTAGGATA 9159
Qy 1437 ACC 1439
Db 9160 ACC 9162

RESULT 13
AAA81489_2/c
Continuation (3 of 9) of AAA81489 from base 200001 (N. meningitidis partial DNA sequence
WP Sequence split into 9 fragments LOCUS AAA81489 Accession AAA81489
WP Fragment Name Begin End
WP AAA81489_0 1 110000
WP AAA81489_1 100001 210000
WP AAA81489_2 200001 310000
WP AAA81489_3 300001 410000
WP AAA81489_4 400001 510000
WP AAA81489_5 500001 610000
WP AAA81489_6 600001 710000
WP AAA81489_7 700001 810000
WP AAA81489_8 800001 837096
Query Match 80.5%; Score 1159; DB 3; Length 110000;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 1286; Conservative 1; Mismatches 147; Indels 9; Gaps 3;
Qy 4 AGAGTTTGTATCCTGGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAAC 63
Db 95302 AGAGTTTGTATCCTGGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAC 95243
Qy 64 GGTATACAGGGTGTCTTGCACCGCTGACGAGTGGCGAAGCGGTGAGTAAATGCGTCG 117
Db 95242 GGCAGCACAGAGAAGCTTGTCTTCCGGTGGCGAGTGGCGAACGGGTGAGTAAACATATCG 95183
Qy 118 GAATGTACCGTGAATATGGGGATAGCTCGCGGAAAGCCGGAATTAATACCGCATACGCCCT 177
Db 95182 GAACGTACCGAGTAGTGGGGATAACTGATCGAAGATCAGCTAAATCCGCATACGCTT 95123
Qy 178 GAGGGGAAGACGGGGATCGAAGACCTCGCGTTATACAGAGCAGCGAGCTCTGATTAG 237
Db 95122 GAGAGAAAGACGGGACCTTCGGGCTTTCGGCTATTCAGCGGCCGATATCTGATTAG 95063
Qy 238 CTAGTTGGTGAAGTAAAGAGTCTACCAAGGGCAGCATCAGTAGCGGGTCTGAGAGGATGAT 297
Db 95062 CTAGTTGGTGAAGGCTTACCAAGGGCAGCATCAGTAGCGGGTCTGAGAGGATGAT 95003
Qy 298 CCGCCACACTGGGACTGAGACACGCGCCAGACTCTACGGGAGGAGGAGTGGGGAATTT 357
Db 95002 CCGCCACACTGGGACTGAGACACGCGCCAGACTCTACGGGAGGAGGAGTGGGGAATTT 94943
Qy 358 TGGACATGGGGCAACCCCTGATCAGCCATGCGCGTGTCTGAAGAGGCTTTCCGGTT 417
Db 94942 TGGACATGGGGCAAGCGCTGATCCAGCATGCGCGTGTCTGAAGAGGCTTTCCGGTT 94883
Qy 418 GTAAAGGACTTTTCTCAGGGAGGAATCCCGCTGGTTAATAACCCGCGGGGATGACAGTA 477
Db 94882 GTAAAGGACTTTTCTCAGGGAGGAATAAGGCTGTTGCTAATATCAGCGGCTGATCAGCGTA 94823
Qy 478 CCBGAAGAATAAGCACCGGCTAACTAGCTGCCAGCAGCCGCGTAATACGTAGGGTGCAA 537
Db 94822 CCBGAAGAATAAGCACCGGCTAACTAGCTGCCAGCAGCCGCGTAATACGTAGGGTGCAA 94763
Qy 538 GCGTTAATCGGAATTACTTGGCGTAAAGCGTCCAGCGGCTTTTGGCAAGTCTGATGTA 597
Db 94762 GCGTTAATCGGAATTACTTGGCGTAAAGCGGCGCAGCGGTACTTAAGCAGAGTGTGA 94703
Qy 598 AAGCCCCGGCTCAACCTTGGGAACGGCATTTGGAGACTGCAAGACTTAGAGTCCGTCAGAGG 657
Db 94702 AATCCCCGGCTCAACCCGGGAATCGCGTTCTGAACCTGGGTGACTCGAGTGTGTCAGAGG 94643
Qy 658 GGGGTAGAAATTCGCGTGTAGCAGTGAATCCGTAGAGATCGGAGGNAATACCGATGGCG 717
Db 94642 GAGGTAGAAATTCACGTGTAGCAGTGAATCCGTAGAGATCGGAGGNAATACCGATGGCG 94583
Qy 718 AAGCAGCCCCCTGGGATGACACTGACGCTCATGCAAGAAAGCGTGGGGAGCAACAGGA 777
Db 94582 AAGCAGCCCTCCTGGGACAACTGACGTTTATGCCCCGAAAGCGTGGGTAGCAACAGGA 94523
Qy 778 TTAGATACCCCTGGTAGTCCAGCCCTAAACGATGTCAATTTAGCTGTTGGG-GGTTTGAAT 836

Db	94522	TTAGATACCCCTGGTAGTCCAGCCCTAAACGATGTCAATTAGCTGTTGGGCAACCTGATT	94463
Qy	837	CCTTGGTAGCTAGCTAACCGGTGAAATTGACCGCTCGGGAGTAGCGCCCAAGGTTAA	896
Db	94462	CCTTGGTAGCTAGCTAACCGGTGAAATTGACCGCTCGGGAGTAGCGTCCCAAGATTAA	94403
Qy	897	AACCTCAAAGGAATTGACGGGACCGCAACAAGCGGTGGATGATGGATTAAATTCGATGC	956
Db	94402	AACCTCAAAGGAATTGACGGGACCGCAACAAGCGGTGGATGATGGATTAAATTCGATGC	94343
Qy	957	AACGGGAAAAACCTTACCTGCTCTTGACATGTACGGAACTTTGGTAGAGATATCTTGGTGC	1016
Db	94342	AACCGGAAGAACCTTACCTGCTCTTGACATGTACGGAACTTTGGTAGAGATATCTTGGTGC	94285
Qy	1017	CCGAAAGGAGCGCTTAACACAGGTGCTGCATGGCTGTGCTCAGCTCGTGTGCTGAGATGT	1076
Db	94284	GCCTTCGGGAGCGGTAAACAGGTGCTGCATGGCTGTGCTCAGCTCGTGTGCTGAGATGT	94225
Qy	1077	TGGGTTAAGTCCCGCAACGAGCGCAACCTTTGTCAATTAGTTGCCATCAATTTAGTTGGGCA	1136
Db	94224	TGGGTTAAGTCCCGCAACGAGCGCAACCTTTGTCAATTAGTTGCCATCAATTTAGTTGGGCA	94165
Qy	1137	CTCTAATGAGACTGCGCGGTGACAAACCGGAGGAGTGGGATGACGTCGAAGTCTCTCATG	1196
Db	94164	CTCTAATGAGACTGCGCGGTGACAAACCGGAGGAGTGGGATGACGTCGAAGTCTCTCATG	94105
Qy	1197	GCCCTTATGACGAGCGGCTTACACGTGCATCAATGCTCGGTACAGAGGTCGCTAAGCCG	1256
Db	94104	GCCCTTATGACGAGCGGCTTACACGTGCATCAATGCTCGGTACAGAGGTCGCTAAGCCG	94045
Qy	1257	CGAGGTGGTCCCAATCTCATAAAACCGATCGTAGTCCGGATCGCACTCTGCAACTCGAGT	1316
Db	94044	CGAGGTGGTCCCAATCTCATAAAACCGATCGTAGTCCGGATCGCACTCTGCAACTCGAGT	93985
Qy	1317	GCCTGAAGTCGGAATCGCTAGTAATCGCAGATCAGCATGCTGCGGTGAATACGTTCCCGG	1376
Db	93984	GCATGAAGTCGGAATCGCTAGTAATCGCAGATCAGCATGCTGCGGTGAATACGTTCCCGG	93925
Qy	1377	GTCTTTGACACACCGCGCTCACACCATGGGAGTGAGTTTCACACAGAGTGGGTAGGCTA	1436
Db	93924	GTCTTTGACACACCGCGCTCACACCATGGGAGTGAGTTTCACACAGAGTGGGTAGGATA	93865
Qy	1437	ACC 1439	
Db	93864	ACC 93862	
RESULT 14			
AAA81489_6/c			
Continuation (7 of 9) of AAA81489 from base 600001 (N. meningitidis partial DNA sequence			
WP Sequence split into 9 fragments LOCUS AAA81489 Accession Aaa81489			
WP	Fragment Name	Begin	End
WP	AAA81489_0	1	110000
WP	AAA81489_1	100001	210000
WP	AAA81489_2	200001	310000
WP	AAA81489_3	300001	410000
WP	AAA81489_4	400001	510000
WP	AAA81489_5	500001	610000
WP	AAA81489_6	600001	710000
WP	AAA81489_7	700001	810000
WP	AAA81489_8	800001	837096
Query Match 80.5%; Score 1159; DB 3; Length 110000;			
Best Local Similarity 89.1%; Pred. No. 0;			
Matches 1286; Conservative 1; Mismatches 147; Indels 9; Gaps 3;			
Qy	4	AGAGTTTGATCCTGGCTCAGATTGAACGCTCGGGCATGCTTTACACATGCAAGTCCGAAC	63
Db	102173	AGAGTTTGATCCTGGCTCAGATTGAACGCTCGGGCATGCTTTACACATGCAAGTCCGAC	102114
Qy	64	GGTA-----ACAGGTGCTTGGACCGGTACGAGTGGCGAAGCGGTGAGTAATGCGTCG	117
Db	102113	GGCAGCACAGAGAAGCTTGCTTCTCGGTGGCGAGTGGCGAAGCGGTGAGTAATGCGTCG	102054

Qy	118	GAATGTACCTGTAAATCGGGGATAGCTCGCGAAAGCCGGATTAAATACCGCATACGCCCT	177
Db	102053	GAACGTACCGAGTAGTGGGGGATACCTGATCGAAAGATACGATTAATACCGCATACGCTT	101994
Qy	178	GAGGGGAAAGCGGGGATCGAAAGACCTCGCGTTATACGAGCAGCCGACGCTCGATTAG	237
Db	101993	GAGAGAAAAGCAGGGGACCTTCGGGCTTTCGCTATTTCGAGCGCGCATATCTGATTAG	101934
Qy	238	CTAGTTGGTAGGTAAAGACTCACCRAAGGCGACGATCAGTAGCGGGTCTGAGAGATGAT	297
Db	101933	CTAGTTGGTAGGTAAAGGCTTACCAAGGCGACGATCAGTAGCGGGTCTGAGAGATGAT	101874
Qy	298	CCGCCACACTGGGACTGAGACACGGCCAGACTCTACGGGAGGACGAGTGGGGAAATTT	357
Db	101873	CCGCCACACTGGGACTGAGACACGGCCAGACTCTACGGGAGGACGAGTGGGGAAATTT	101814
Qy	358	TGACAAATGGGGGCAACCCCTGATCCAGCCATGCGCGTGTCTGAAGAGCGCTTCGGGTT	417
Db	101813	TGACAAATGGGGGCAACCCCTGATCCAGCCATGCGCGTGTCTGAAGAGCGCTTCGGGTT	101754
Qy	418	GTAAGGACTTTTGTACGGGAGGAAATCCCGCTGGTTAATACCCGCGGGGATACAGTA	477
Db	101753	GTAAGGACTTTTGTACGGGAGGAAATCCCGCTGGTTAATACCCGCGGGGATACAGTA	101694
Qy	478	CCBGAAGAAATAAGCACCGGCTAACTACGTGCAGCAGCCGCGTAAATACGTAGGCTGCAA	537
Db	101693	CCTGAAGAAATAAGCACCGGCTAACTACGTGCAGCAGCCGCGTAAATACGTAGGCTGCAA	101634
Qy	538	GCCTTAATCGGAATTAATCTGGGCGTAAAGCGTGCAGCGCGGTTTTCGAAGTCTGATGTA	597
Db	101633	GCCTTAATCGGAATTAATCTGGGCGTAAAGCGGCGCAGACGGTTACTTTAAGCAGGATGTA	101574
Qy	598	AAGCCCCGGGCTCAACTGGGAAACCGCATTTGGAGACTGCAAGACTAGAGTCCGTACAGG	657
Db	101573	AATCCCCGGGCTCAACCCGGGAACTGCGTTCTGAACCTGGGTGACTCGAGTGTGTACAGG	101514
Qy	658	GGGTAGAAATTCGCGGTGTAGCAGTGAATTCGCTAGAGATGCGGAGGAATACCGATGGCG	717
Db	101513	GAGGTAGAAATTCACGTGTAGCAGTGAATTCGCTAGAGATGCGGAGGAATACCGATGGCG	101454
Qy	718	AAGCAGCCCCCTGGGATGACATGACGCTCATGCACGAAGCGTGGGGAGCAACAGGA	777
Db	101453	AAGCAGCCCCCTGGGATGACATGACGCTCATGCACGAAGCGTGGGTAGCAACAGGA	101394
Qy	778	TTAGATACCTCTGTAGTCCACGCGCTTAAACGATGTCAATTTAGCTGTGGG--GGTTGAT	836
Db	101393	TTAGATACCTCTGTAGTCCACGCGCTTAAACGATGTCAATTTAGCTGTGGGCAACCTGAT	101334
Qy	837	CCTTGGTAGCTAGCTAACCGGTGAAATTCACCGCTGGGGAGTACCGCGCAAGGTTAA	896
Db	101333	CCTTGGTAGCTAGCTAACCGGTGAAATTCACCGCTGGGGAGTACCGTGCAGAGATTAA	101274
Qy	897	AACCTCAAAGGAATTGACGGGACCCCGCACAAAGCGGTGGATGATGGATTAAATTCGATGC	956
Db	101273	AACCTCAAAGGAATTGACGGGACCCCGCACAAAGCGGTGGATGATGGATTAAATTCGATGC	101214
Qy	957	AACCGGAAAAACCTTACCTGCTCTTGACATGTACGGAACCTTGGTAGAGATATCTTGGTGC	1016
Db	101213	AACCGGAAAGAACCTTACCTGCTCTTGACATGTACGGAACCTTGGTAGAGATATCTTGGTGC	101156
Qy	1017	CCGAAAGGAGCGGTAAACAGGTGCTGCATGGCTGTGCTGCTGCTGCTGCTGAGATGT	1076
Db	101155	GCCTTCGGGAGCGGTAAACAGGTGCTGCATGGCTGTGCTGCTGCTGCTGAGATGT	101096
Qy	1077	TGGTTTAAGTCCCGCAACGAGCGCAACCCCTTGTCAATTAGTTGCCATCAATTTAGTTGGGCA	1136
Db	101095	TGGTTTAAGTCCCGCAACGAGCGCAACCCCTTGTCAATTAGTTGCCATCAATTTAGTTGGGCA	101036
Qy	1137	CTCTAATGAGACTGCGCGGTGACAAAACGGAGGAAGGTGGGGATGACGTCAAGTCTCATG	1196
Db	101035	CTCTAATGAGACTGCGCGGTGACAAAACGGAGGAAGGTGGGGATGACGTCAAGTCTCATG	100976

QY	1197	GCCTTATGACGAGGCTTCACAGTCTATCAATGGTCGGTACAGAGGTCGCTAAGCCG	1256
Db	100975	GCCTTATGACGAGGCTTCACAGTCTATCAATGGTCGGTACAGAGGTCGCTAAGCCG	100916
QY	1257	CGAGTGGTGCAATCTCATAAAAACCGATCGTAGTCCGGATCGCACTCTGCAACTCGAGT	1316
Db	100915	CGAGCGAGCAATCTCACAACCGATCGTAGTCCGGATCGCACTCTGCAACTCGAGT	100856
QY	1317	CGGTGAAGTCGGAATCGTAGTAATCGCAGATCAGCATGCTGCGGTGAATACGTTCCGG	1376
Db	100855	GCATGAAGTCGGAATCGTAGTAATCGCAGTACGATACCTGCGGTGAATACGTTCCGG	100796
QY	1377	GTCCTGTACACACGCCCGTCACACCATGGAGTGGGGATACACAGAGTGGTAGGTA	1436
Db	100795	GTCCTGTACACACGCCCGTCACACCATGGAGTGGGGATACACAGAGTGGTAGGTA	100736
QY	1437	ACC 1439	
Db	100735	ACC 100733	
RESULT 15			
AAA81489_7/c			
Continuation (8 of 9) of AAA81489 from base 700001 (N. meningitidis partial DNA sequence)			
WP Sequence split into 9 fragments LOCUS AAA81489 Accession Aaa81489			
WP	Fragment Name	Begin	End
WP	AAA81489_0	1	110000
WP	AAA81489_1	100001	210000
WP	AAA81489_2	200001	310000
WP	AAA81489_3	300001	410000
WP	AAA81489_4	400001	510000
WP	AAA81489_5	500001	610000
WP	AAA81489_6	600001	710000
WP	AAA81489_7	700001	810000
WP	AAA81489_8	800001	837096
Query Match			
Best Local Similarity 80.5%; Score 1159; DB 3; Length 110000;			
Matches 1286; Conservative 1; Mismatches 147; Indels 9; Gaps 3;			
QY	4	AGAGTTTATCTCGCTCAGATTGAACGCTGGCGCATGCTTTACATGCAAGTCGAAC	63
Db	2173	AGAGTTTATCTCGCTCAGATTGAACGCTGGCGCATGCTTTACATGCAAGTCGGAC	2114
QY	64	GGTA-----ACAGGGTGCTTGCAACCGTGACAGTGGCGAACCGGTGAGTAATCGGTG	117
Db	2113	GGCAGCACAGAGAAGCTTGCTTCTCGGGTGGCGAGTGGCGAACCGGTGAGTAACATATCG	2054
QY	118	GAATGTACCGTGTAAATGGGGATAGCTCGGCGAAGCCGGATTATACCGCATACGCCCT	177
Db	2053	GAACGTACCGAGTAGTGGGGGATACTGATCGAAAGATCAGCTAATACCGCATACGCTTT	1994
QY	178	GAGGGGAAAGCGGGGATCGAAAGACCTTCGGCTTATACGAGCAGCCGACGCTCGATTAG	237
Db	1993	GAGAGAAAGCAGGGACCTTCGGCCCTTGCGCTATTCGAGCGCCGATATCTGATTAG	1934
QY	238	CTAGTTGTGAGGTAAAGACTCACCAAGCGACGATCAGTAGTCCGGGTCTGAGAGGATGAT	297
Db	1933	CTAGTTGTGGGTAAAGCCCTACCAAGCGACGATCAGTAGTCCGGGTCTGAGAGGATGAT	1874
QY	298	CCGCCACACTGGGACTGAGACACGCCACGACTCTACGGGAGGACGAGTCGGGAATTT	357
Db	1873	CCGCCACACTGGGACTGAGACACGCCACGACTCTCTACGGGAGGACGAGTCGGGAATTT	1814
QY	358	TGGCAATGGGGCAACCCCTGATCCAGCCATCGCCGCTGTCTGAAAGAGGCCCTTCGGGTT	417
Db	1813	TGGCAATGGGGCAAGCCTGATCCAGCCATCGCCGCTGTCTGAAAGAGGCCCTTCGGGTT	1754
QY	418	GTAAGGACTTTTGTGAGGAGGAATCCCGCTGGTTAATACCCGGCGGGGATGACAGTA	477
Db	1753	GTAAGGACTTTTGTGAGGAGGAATCCCGCTGGTTAATACCCGGCGGGTGTGACGGTA	1694
QY	478	CCBGAAGATAGCACCGGCTTAACGTACGTGCCAGCAGCGCGGTAAATACGTAGGGTGC	537

Search completed: May 23, 2006, 23:28:15
Job time : 985 secs

Db	1693	CCTGAGAAATAGCACCGGCTAACTAGTGCAGACGCCGGTAAATACGTAGGTCGGA	1634
QY	538	GCCTTAATCGGAATTAATCTGGCGTAAAGCGTGCAGCGGTTTTGCAAGTCTGATGTA	597
Db	1633	GCCTTAATCGGAATTAATCTGGCGTAAAGCGGCGCAGACGTTACTTTAAGCAGGATGTA	1574
QY	598	AAGCCCGGCTCAACCTGGGAACGGCATTTGGAGACTGCAAGACTAGAGTCGTCAGAGG	657
Db	1573	AATCCCGGGCTCAACCCGGAACTGCGTTCTGNACTTGGGTGACTCGAGTGTGACAGG	1514
QY	658	GGGTAGAAATTCGCGGTGTAGCAGTGAATTCGCTAGAGATCGCGAGGAATACCGATGCG	717
Db	1513	GAGGTAGAAATTCACGCTGTAGCAGTGAATTCGCTAGAGATGTGAGGAATACCGATGCG	1454
QY	718	AAGCAGCCCGCTGGGATGACATGACGCTCATGCAAGAAAGCGTGGGAGCAACAGGA	777
Db	1453	AAGCAGCCCTCTGGGACAACTGACGTTTCAATGCCGGAAGCGTGGGTAGCAACAGGA	1394
QY	778	TTAGATACCCCTGGTAGTCCACGCCCTAAACGATGCTCAATTAGCTGTTGGG-GGTTTGAAT	836
Db	1393	TTAGATACCCCTGGTAGTCCACGCCCTAAACGATGCTCAATTAGCTGTTGGGCAACCTGATT	1334
QY	837	CCTTGGTAGCTAGCTAAACGCGTGAAATTTGACCCGCTGGGAGTACGCGCAAGGTTAA	896
Db	1333	GCTTGGTAGCTAGCTAAACGCGTGAAATTTGACCCGCTGGGAGTACGCGTCAAGATTAA	1274
QY	897	AACCTCAAAGGAATTTGACGGGACCCGCAAGCGGTGATGATGGAATTAATTCGATGC	956
Db	1273	AACCTCAAAGGAATTTGACGGGACCCGCAAGCGGTGATGATGGAATTAATTCGATGC	1214
QY	957	AACCGGAAGAACCTTACTGCTCTTTGACATGTCGGAACCTTGGTAGAGATATCTTGGTGC	1016
Db	1213	AACCGGAAGAACCTTACTGCTCTTTGACATGTCGGA--TCCTCCGAGACGGAGGAGT	1156
QY	1017	CCGAAAGGAGCCGTAACACAGGTGCTGCATGCTGCTGCTGCTGCTGCTGCTGCTGATGT	1076
Db	1155	GCCTTGGGAGCCGTAAACACAGGTGCTGCATGCTGCTGCTGCTGCTGCTGCTGATGT	1096
QY	1077	TGGGTAAAGTCCCGAACAGAGCGCAACCTTTGTCATTTAGTTGCCATCATTTAGTTGGCA	1136
Db	1095	TGGGTAAAGTCCCGAACAGAGCGCAACCTTTGTCATTTAGTTGCCATCATTTAGTTGGCA	1036
QY	1137	CTCTAATGAGACTGCCGGTGAACCGGAGGAAGTGGGATGACGTCAAGTCTCTCATG	1196
Db	1035	CTCTAATGAGACTGCCGGTGAACCGGAGGAAGTGGGATGACGTCAAGTCTCTCATG	976
QY	1197	GCCCTTATGACGAGGCTTTCACAGCTCATACAATGGTGGTACAGAGGTCGCTAAGCCG	1256
Db	975	GCCCTTATGACGAGGCTTTCACAGCTCATACAATGGTGGTACAGAGGTCGCTAAGCCG	916
QY	1257	CGAGGTGTGCAATCTCATAAAACCGATCGTAGTCCGGATCGCACCTGCAACTCGAGT	1316
Db	915	CGAGGTGTGCAATCTCATAAAACCGATCGTAGTCCGGATCGCACCTGCAACTCGAGT	856
QY	1317	CGGTGAAGTCCGGAATCGTAGTAATCGCAGATCAGCATGCTGCGGTGAATACGTTCCCG	1376
Db	855	GCATGAAGTCCGGAATCGTAGTAATCGCAGGTGACATACCTGCGGTGAATACGTTCCCG	796
QY	1377	GTCCTGTACACACCGCCGTCACACCATGGAGTGAAGTTTCAACAGAAAGTGGGTAGGCTA	1436
Db	795	GTCCTGTACACACCGCCGTCACACCATGGAGTGGGGATACACAGAAAGTAGGTAGGATA	736
QY	1437	ACC 1439	
Db	735	ACC 733	

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2006, 00:50:35 ; Search time 1994 Seconds
(without alignments)

8873.719 Million cell updates/sec

Title: US-10-678-023A-1

Perfect score: 1439.2

Sequence: 1 tggagagttgtatcctggctt.....agaagtggtaggtaaccg 1440

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA Main:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1439.2	100.0	1440	US-10-678-023-1	Sequence 1, Appli
2	1180	82.0	1522	US-11-198-242-2	Sequence 2, Appli
3	1169.6	81.3	1610	US-10-029-397A-43	Sequence 43, Appli
4	1165.8	81.0	1460	US-10-168-337A-6	Sequence 6, Appli
5	1161.6	80.7	1532	US-10-029-397A-38	Sequence 38, Appli
6	1160.6	80.6	1460	US-10-168-337A-4	Sequence 4, Appli
7	1159.8	80.6	1488	US-10-029-397A-42	Sequence 42, Appli
8	1159	80.5	1460	US-10-168-337A-2	Sequence 2, Appli
9	1159	80.5	1544	US-10-029-397A-45	Sequence 45, Appli
10	1159	80.5	2242716	US-10-915-740A-1068	Sequence 1068, Ap
11	1159	80.5	2242716	US-10-915-740A-1068	Sequence 1068, Ap
12	1157.6	80.4	1460	US-10-168-337A-1	Sequence 1, Appli
13	1152	80.0	1544	US-09-726-774-5	Sequence 5, Appli
14	1152	80.0	1544	US-10-029-397A-44	Sequence 44, Appli
15	1152	80.0	1544	US-10-719-633-5	Sequence 5, Appli
16	1150	79.9	1459	US-10-168-337A-8	Sequence 8, Appli
17	1149.8	79.9	1478	US-10-168-337A-3	Sequence 3, Appli

18	1149	79.8	1458	8	US-10-659-948A-3	Sequence 3, Appli
19	1149	79.8	1458	8	US-10-659-980A-3	Sequence 3, Appli
20	1149	79.8	1458	8	US-10-659-983A-3	Sequence 3, Appli
21	1148.4	79.8	1426	7	US-10-168-337A-9	Sequence 9, Appli
22	1147.6	79.7	1464	7	US-10-029-397A-40	Sequence 40, Appli
23	1147.6	79.7	1485	7	US-10-168-337A-10	Sequence 10, Appli
24	1146.8	79.7	1535	7	US-10-029-397A-41	Sequence 41, Appli
25	1137	79.0	1485	7	US-10-029-397A-39	Sequence 39, Appli
26	1135	78.9	20844	10	US-10-915-740A-8	Sequence 8, Appli
27	1126.8	78.3	1496	10	US-10-723-365B-32	Sequence 32, Appli
28	1126	78.2	1530	9	US-10-875-161-1	Sequence 1, Appli
29	1124	78.1	1526	16	US-11-198-242-1	Sequence 1, Appli
30	1119.4	77.8	1508	16	US-11-248-383-1	Sequence 1, Appli
31	1118.6	77.7	1451	7	US-10-219-549-1	Sequence 1, Appli
32	1115.6	77.5	1491	8	US-10-659-948A-20	Sequence 20, Appli
33	1115.6	77.5	1491	8	US-10-659-980A-20	Sequence 20, Appli
34	1115.6	77.5	1491	8	US-10-659-983A-20	Sequence 20, Appli
35	1104.4	76.7	1494	8	US-10-659-948A-19	Sequence 19, Appli
36	1104.4	76.7	1494	8	US-10-659-980A-19	Sequence 19, Appli
37	1104.4	76.7	1494	8	US-10-659-983A-19	Sequence 19, Appli
38	1103	76.6	1457	8	US-10-659-948A-1	Sequence 1, Appli
39	1103	76.6	1457	8	US-10-659-980A-1	Sequence 1, Appli
40	1103	76.6	1457	8	US-10-659-983A-1	Sequence 1, Appli
41	1099.8	76.4	1457	8	US-10-659-948A-2	Sequence 2, Appli
42	1099.8	76.4	1457	8	US-10-659-980A-2	Sequence 2, Appli
43	1099.8	76.4	1457	8	US-10-659-983A-2	Sequence 2, Appli
44	1098.4	76.3	1467	8	US-10-659-948A-18	Sequence 18, Appli
45	1098.4	76.3	1467	8	US-10-659-980A-18	Sequence 18, Appli

ALIGNMENTS

RESULT 1

US-10-678-023-1

; Sequence 1, Application US/10678023

; Publication No. US20050074431A1

; GENERAL INFORMATION:

; APPLICANT: Martin et al., Phyllis A. W.

; TITLE OF INVENTION: CHROMOBACTERIUM SUTTSUGA SP. NOV. AND USE FOR CONTROL OF INSECT

; FILE REFERENCE: 0136.02

; CURRENT APPLICATION NUMBER: US/10/678,023

; CURRENT FILING DATE: 2003-10-01

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: Patentin version 3.2

; SEQ ID NO 1

; LENGTH: 1440

; TYPE: DNA

; ORGANISM: Chromobacterium suttsuga NRRL B-30655

US-10-678-023-1

Query Match 100.0%; Score 1439.2; DB 10; Length 1440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TGGAGAGTTTGATCCTGGCTCAGATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCG	60
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QY	61	AACGGTAAACAGGGTGTCTTCACCGCTGACGAGTGGCGAAACGGGTGAGTAAATGCGTCGGAA	120
Db	61	AACGGTAAACAGGGTGTCTTCACCGCTGACGAGTGGCGAAACGGGTGAGTAAATGCGTCGGAA	120
QY	121	TGTACCGTGTAAATGGGGGATAGCTCGCGAAACCGGATTAATACCGCATACGCCCTGAG	180
Db	121	TGTACCGTGTAAATGGGGGATAGCTCGCGAAACCGGATTAATACCGCATACGCCCTGAG	180
QY	181	GGGGAAGCGGGGATCGAAAGACCTCGCGTTATACGACGACCGACGCTCTGATTAGCTA	240
Db	181	GGGGAAGCGGGGATCGAAAGACCTCGCGTTATACGACGACCGACGCTCTGATTAGCTA	240
QY	241	GTTGGTGAAGAGCTCAACCAAGCGCAGCATGAGTAGGGGTCTGAGAGGATGATCCG	300

Db 241 GTTGGTGGGTAAGAGCTCACCAAGGCGACGATCAGTAGCCGGTCTGAGAGGATGATCCG 300
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Db 301 CCACACTGGGACTGAGACACGCGCCAGACTCCTACGGGAGGACAGTGGGGAAATTTGG 360
Qy |||||||
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Qy |||||||
Db 361 ACAATGGGGCAACCTTGATCCAGCATGCGCGCTGTCTGAAGAAGCCCTTCGGGTTGTA 420
Qy |||||||
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Qy |||||||
Db 421 AAGGACTTTTCTCAGGAGGAAATCCGCTGTTTAATACCGCGGGGATGACAGTACCB 480
Qy |||||||
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Qy |||||||
Db 481 GAAGAATAAGCACCGGCTAACTAGTGTCCAGCAGCGCGGTAAATACGTAGGGTCAAGCG 540
Qy |||||||
Db 481 GAAGAATAAGCACCGGCTAACTAGTGTCCAGCAGCGCGGTAAATACGTAGGGTCAAGCG 540
Qy |||||||
Db 541 TTAATCGGAATTAATCTGGGCGTAAAGCGTGCAGCGGCTTTTGCAGTCTGATGTAAAG 600
Qy |||||||
Db 541 TTAATCGGAATTAATCTGGGCGTAAAGCGTGCAGCGGCTTTTGCAGTCTGATGTAAAG 600
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Db 601 CCCCGGCTCAACCTGGGAACGGCATTTGGAGACTGCAAGACTAGAGTGCCTCAGAGGGG 660
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Db 721 GCAGCCCTCGGATGACACTGACCTCATGCAAGCAAGCGTGGGAGCAACAGGATTA 780
Qy |||||||
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Db 1081 TTAAGTCCCGCAACGAGCGCAACCTTGTTCATTAGTTGCCATCAATTTAGTTGGGCACTCT 1140
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Db 1141 AATGAGACTGCCGGTGACAAACCGGAGGAAGTGGGGATGAGCTCAAGTCTCATGGGCC 1200
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Db 1201 TTATGAGCAGGGCTTTCACACGTCATACAAATGGTCCGTAACAGAGGTCTCAAGCCGAG 1260
Qy |||||||
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Db 1261 GTGGTCCCAATCTCATAAACCGATCGTAGTCCGATCGCACTCTGCAACTCGAGTGGGT 1320
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Db 1321 GAAGTCGGAATCGCTAGTAAATCGCAGATCAGCATGCTGCGGTGAATACGTTCCCGGTCT 1380
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Db 1381 TGTACACACCGCCCGTCAACACCTGGAGTGGAGTGTGTTTACCCAGAGTGGGTAGGCTAACCG 1440
Qy |||||||
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Qy |||||||

RESULT 2
US-11-198-242-2
; Sequence 2, Application US/11198242
; Publication No. US20060035345A1
; GENERAL INFORMATION:
; APPLICANT: AJINOMOTO CO., INC.
; TITLE OF INVENTION: Process for the production of beta-amino acids by using acylase
; FILE REFERENCE: AB04037
; CURRENT APPLICATION NUMBER: US/11/198,242
; CURRENT FILING DATE: 2005-08-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: Burkholderia sp.
; FEATURE:
; NAME/KEY: 16S rDNA
; LOCATION: (1)..(1522)
; OTHER INFORMATION:
; US-11-198-242-2

Query Match 82.0%; Score 1180; DB 16; Length 1522;
Best Local Similarity 89.3%; Pred. No. 0;
Matches 1283; Conservative 1; Mismatches 147; Indels 5; Gaps 1;

Qy 5 GAGTTTCATCTGCTCAGATTGAAACGCTGGCGCATGCTTTTACATGCAAGTCGAACG 64
Db 1 GAGTTTCATCTGCTCAGATTGAAACGCTGGCGCATGCTTTTACATGCAAGTCGAACG 60
Qy 65 GTAACAGGGTCTTTCACCGCTGACAGTGCAGAACCGGTGAGTAATGCGTCGGAATGTA 124
Db 61 GCACGGCGGGGCAACCCCTGGCGCGAGTGGCAACCGGTGAGTAATACATCGGAACGTG 120
Qy 125 CCCTGTAATGGGGATAGCTCGCGAAAGCCGGAATTAATACCGCATACGCCCTCAGGGGG 184
Db 121 TCCTGTAGTGGGGATAGCCCGGAAAGCCGGAATTAATACCGCATACGCCCTCAGGGAG 180
Qy 185 AAACGGGGGATCGAAAGAACCTCGCGTTATACGAGCAGCGACGTCTGATTAGTAGTTG 244
Db 181 AAAGGGGGGATCTTAGGACCTCTCGCTACAGGGGCGGCCGATGGCAGATTAGCTAGTTG 240
Qy 245 GTGAGGTAAGAGCTCACCAAGGCCACGATCAGTAGCGGTCTGAGAGGATCATCCGCCAC 304
Db 241 GTGGGGTAAAGGCCCTTACCAAGGCCACGATCTGTAGCTGGTCTGAGAGGACACCGACAC 300
Qy 305 ACTGGGACTGAGACACCGCCAGACTCCTACGGGAGGAGCAGTGGGGAATTTTGGACAA 364
Db 301 ACTGGGACTGAGACACCGCCAGACTCCTACGGGAGGAGCAGTGGGGAATTTTGGACAA 360
Qy 365 TGGGGCAACCCCTGATCCAGCCATCGCGGTCTGAAGAAGGCCCTTCGGGTTGTAAAGG 424
Db 361 TGGGGCAAGCCCTGATCCAGCAATCGCGGTGTGTGAAGAAGGCCCTTCGGGTTGTAAAGC 420
Qy 425 ACTTTTGTTCAGGGAGGAATCCCGTGTAAATACCGCGGGGATGACAGTACCBGAAG 484
Db 421 ACTTTTGTTCAGGAAGAAACCCCGTGTAAATACCGTGGCGGATGACGTTACCGAAG 480
Qy 485 AATAAGCACCGGCTTAACCTACGTGCCAGCAGCCGCGTAAATACGTAGGGTCAAGCGTTAA 544
Db 481 AATAAGCACCGGCTTAACCTACGTGCCAGCAGCCGCGTAAATACGTAGGGTCAAGCGTTAA 540
Qy 545 TCGGAATTTACTGGGGTAAACCGTGCAGCGCGGTTTTGCAAGTCTGATGTGAAGCCCC 604
Db 541 TCGGAATTTACTGGGGTAAAGCGTGCAGCGCGGTTCGCTAAGACAGATGTAATCCCC 600
Qy |||||||


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Qy 1342 CGCAGATCAGCATCTGCGTGAATAGTTCCGGGTCTTGTATACACACCGCCGTCACAC 1401
Db 1321 CGCGATCAGATGCGCGGTGAATACGTTCCCGGTCTTGTATACACACCGCCGTCACAC 1380
Qy 1402 CATGGAGTCAGTTTACACAGAGTGGTAGCTAACCG 1440
Db 1381 CATGGAGCGGGTTCTGCCAGAGTAGTTAGCCTAACCG 1419

RESULT 5
US-10-029-397A-38
; Sequence 38, Application US/10029397A
; Publication No. US20030175709A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, GEORGE L.
; APPLICANT: WHITLEY, J. PENN
; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS
; FILE REFERENCE: AMBI:076US
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 1532
; TYPE: DNA
; ORGANISM: Bordetella bronchiseptica
US-10-029-397A-38

Query Match      80.7%; Score 1161.6; DB 7; Length 1532;
Best Local Similarity 88.4%; Pred. No. 0;
Matches 1273; Conservative 1; Mismatches 161; Indels 5; Gaps 1;

Qy 1 TGAGAGTTTGATCTCGGCTCAGATTGAACGCTGGCGGATGCTTTACACATCAAGTCG 60
Db 6 TGAGAGTTTGATCTCGGCTCAGATTGAACGCTGGCGGATGCTTTACACATCAAGTCG 65
Qy 61 AACGGTAACAGGTGCTTGACCGCTGACAGTGGCGAAGCGGTGAGTAAATGCGTCGAA 120
Db 66 GACGGCAGCACGGGCTTCGGCTGCTGGCGAGTGGCGAAGCGGTGAGTAAATGTCGAA 125
Qy 121 TGTAACGTGTAATGGGGATAGCTCGCGAAGACCGGATTAATACCGCATACGCCCTGAG 180
Db 126 CGTGCCCACTAGAGCGGGGATAACTACCGAAGCGTGGCTTAATACCGCATACGCCCTAG 185
Qy 181 GGGAAAGCGGGGATCGAAGACCTCGCGTTATACGAGCAGCGGACGCTCTGATTAGCTA 240
Db 186 GGGAAAGCGGGGACCTTCGGGCTTCGCACTATTGGAGCGGCCGATATCGGATTAGCTA 245
Qy 241 GTTGGTGAAGTAAGAGCTCACCAAGGCGACGATCAGTAGCGGTCTGAGAGGATGATCCG 300
Db 246 GTTGGTGGGTAAACGGCTTACCAAGGCGACGATCCGTTAGTGGTTGAGAGGACGACAG 305
Qy 301 CCACACTGGGACTGAGACACCGGCCAGACTCCTACGGGAGGCGAGTGGGGAATTTGG 360
Db 306 CCACACTGGGACTGAGACACCGGCCAGACTCCTACGGGAGGCGAGTGGGGAATTTGG 365
Qy 361 ACAATGGGGCAACCTGTATCCAGCGCATCGCGGTGCTGGAAGACGCTTCGGGTGTGA 420
Db 366 ACAATGGGGCAACCTGTATCCAGCCATCCCGGTGTGCGATGAAGCCCTTCGGGTGTGA 425
Qy 421 AAGGACTTTTGTGAGGAGGAAATCCCGTGTGTTAATACCCGCGGGGATGACAGTACCB 480
Db 426 AAGCACTTTTGGCAGGAAAGAAACGGCAGCGGTATATCTCTGCAACTGACGGTACCT 485
Qy 481 GAAGATAAGCACCGGCTAAGTACGTGCGAGAGCGCGGTATATACGTAGGTGCAAGCG 540
Db 486 GCAGATAAGCACCGGCTAAGTACGTGCGAGAGCGCGGTATATACGTAGGTGCAAGCG 545
Qy 541 TTAATCGGAATTACTGGCGCTAAGCGTGCAGCGGCTTTTCCAAAGTCTGATGCAAG 600
Db 546 TTAATCGGAATTACTGGCGCTAAGCGTGCAGCGGCTTTTCCAAAGTCTGATGCAAG 605
Qy 601 CCCCGGGCTCAACCTGGGAACGGCATTTGGAGACTGCAAGACTAGAGTGGCTCAGAGGGG 660
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Db 606 CCAGGGCTTAACCTTGGAACTGCATTTTAACTACCGGCTAGAGTGTCTCAGAGGAG 665
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Db 666 GTGGAATTCCTCGGCTGAGCAGTGAATGCGTAGATATCGGAGGAACACCGATGGCGAAG 725
Qy 721 GCAGCCCCCTGGGATGACACTGACGCTCATGACAAAGCGTGGGAGCAAAACAGGATTA 780
Db 726 GCAGCCCTCTGGGATAACACTGACGCTCATGACAAAGCGTGGGAGCAAAACAGGATTA 785
Qy 781 GATACCTCTGTAGTCCACGCCCTAAACGATGCAATAGCTGTGGGGTGTGAATCTCTT 840
Db 786 GATACCTCTGTAGTCCACGCCCTAAACGATGCAATAGCTGTGGGGTGTGAATCTCTT 845
Qy 841 GGTAGCGTAGCTAAACGCGTGAATTTGACCGCTGGGAGTACGCGCGCAAGGTTAAACT 900
Db 846 GGTAGCGTAGCTAAACGCGTGAATTTGACCGCTGGGAGTACGCGCGCAAGGTTAAACT 905
Qy 901 CAAAGGAATTGACGGGGACCCGCAAGCGGTGGATGATGTGATTAATTCGATGCAACG 960
Db 906 CAAAGGAATTGACGGGGACCCGCAAGCGGTGGATGATGTGATTAATTCGATGCAACG 965
Qy 961 CGAAAAAACCCTTACCTGCTCTTGACATGTACGGAACCTTGGTAGAGATATCTTGGTGC CGA 1020
Db 966 CGAAAAAACCCTTACCTGCTCTTGACATGTCTGGAATCCCGAAGAGATTTGGGAGTGTGCG 1025
Qy 1021 AAGGAGCGGTAAACACAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db 1026 AAGGAGCGGTAAACACAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1085
Qy 1081 TTAAGTCCCGCAACGAGCGCAACCCCTTGTCAATTAGTTGCCATCATTTAGTTGGGCACTCT 1140
Db 1086 TTAAGTCCCGCAACGAGCGCAACCCCTTGTCAATTAGTTGGTACGAA- - - - -GGGCACTCT 1140
Qy 1141 AATGAGACTGCGCGGTGACAAACCGGAGGAAGGTGGGATGACGTCGAAGTCTCTATGSCCC 1200
Db 1141 AATGAGACTGCGCGGTGACAAACCGGAGGAAGGTGGGATGACGTCGAAGTCTCTATGSCCC 1200
Qy 1201 TTATGAGCAGGGCTTCACACGTCATACAAATGTCGCTGAGAGGTCGCTTAAGCCCGAG 1260
Db 1201 TTATGAGTGGGCTTCACACGTCATACAAATGTCGCGGACAGAGGTCGCGCAACCCGAG 1260
Qy 1261 GTGGTGCCTAATCTCATAAACCGATCGTAGTCCGATCCGACTCTCGCAACTCGAGTCCGT 1320
Db 1261 GGGAGCCATCCAGAAACCCGATCGTAGTCCGATCCGACTCGAGTCTGCAACTCGACTGCGT 1320
Qy 1321 GAAGTCGGAATCGCTAGTAATCGAGATCAGCATGCTGCGGTGAATACGTTCCCGGTCT 1380
Db 1321 GAAGTCGGAATCGCTAGTAATCGCGATCAGCATGTCGCGGTGAATACGTTCCCGGTCT 1380
Qy 1381 TGTACACACCGCCGTCACACCATGGAGTGGATTTTACCAGAAAGTGGTAGGCTAACCG 1440
Db 1381 TGTACACACCGCCGTCACACCATGGAGTGGATTTTACCAGAAAGTGGTAGGCTAACCG 1440

RESULT 6
US-10-168-337A-4
; Sequence 4, Application US/10168337A
; Publication No. US20030170654A1
; GENERAL INFORMATION:
; APPLICANT: Crocetti, Gregory R.; Tyson, Gene W.; Hugenholtz, Philip; and Blackall,
; APPLICANT: Linda L.
; TITLE OF INVENTION: Probes and Primers for the Detection of Polyphosphate
; FILE REFERENCE: 002367PC/KF
; CURRENT FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1460
; TYPE: DNA
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; ORGANISM: Rhodocyclus tenuis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1045, 1315
; OTHER INFORMATION: n = unknown
US-10-168-337A-4

Query Match      80.6%; Score 1160.6; DB 7; Length 1460;
Best Local Similarity 89.0%; Pred. No. 0;
Matches 1263; Conservative 1; Mismatches 153; Indels 2; Gaps 1;

Qy 24 ATTGAACCGCTGGCGGCATGCTTTACACATCGAAGTCGAACGGTAAACAGGGTGCTTGACCC 83
Db 1 ATTGAACCGCTGGCGGCATGCTTTACACATCGAAGTCGAACGGTAAACAGGGTGCTTGACCC 60
Qy 84 GCTGACAGTGGGAAACGGGTGAGTAATGCGTGGAAATGACCGTGTAAATGGGGATGAC 143
Db 61 GGTGGAGTGGGAAACGGGTGAGTAATGCGTGGAAATGACCGTGTAAATGGGGATGAC 120
Qy 144 TCGCGGAAAGCCGATTAATACCGCATACGCCCTGAGGGGAAAGCGGGGATCGAAGA 203
Db 121 GTAGCGAAAGTTACGCTTAATACCGCATATTTCTGTGAGCAGGAAGACAGGGGATCGAAGA 180
Qy 204 CCTCGCGTTATACGAGCAGCGCAGCTCTGATTAGCTAGTTGGTGGGTAAAGAGCTCACCA 263
Db 181 CCTTGCCTTTGGAGCGCGCATGTCCGATTAGCTAGTTGGTGGGTAAAGAGCTCACCA 240
Qy 264 AGGCGACGATCAGTAGCGGGTCTGAGAGGATGATCCGCCACACTGGGACTGAGACACGGC 323
Db 241 AGGCCACGATCCGTAGCGGGTCTGAGAGGATGATCCGCCACACTGGGACTGAGACACGGC 300
Qy 324 CCAGACTCTACGGGAGCGCAGCTGGGAAATTTTGACAAATGGGGCAACCTGTATCCA 383
Db 301 CCAGACTCTACGGGAGCGCAGCTGGGAAATTTTGACAAATGGGGCAACCTGTATCCA 360
Qy 384 GCCATGCGCGTGTCTGAAGAAGCCCTTCGGGTGTAAAGCACTTTGTGAGGAGGAAA 443
Db 361 GCCATGCGCGTGTAGTGAAGAGCCCTTCGGGTGTAAAGCACTTTTCGGGGGAGAAA 420
Qy 444 TCCCGCTGGTTAATACCGCGGGGATGACAGTACCBGAAGAAATGAAGACCGGTAACTA 503
Db 421 TTGCTCAGGATAATACCTCAGTAGATGACGGTACCCGGAAGAAAGACCGGTAACTA 480
Qy 504 CGTCCAGCAGCCCGGTATACCTAGGTGCAAGCTTAATCGGAATTAATCGGGCTGAA 563
Db 481 CGTCCAGCAGCCCGGTATACCTAGGTGCAAGCTTAATCGGAATTAATCGGGCTGAA 540
Qy 564 AGCGTGGCGAGCGGTTTTCGAAGTCTGATGTGAAGCCCGGGCTCAACCTGGGAACGG 623
Db 541 AGCGTGGCGAGCGGTTTTCGAAGCAGACAGCTGAATCCCGGGCTCAACCTGGGAACGT 600
Qy 624 CATTGGAGACTGCAAGACTAGAGTCGTCAGAGGGGGTAGAATTCGCGTGTAGCAGTG 683
Db 601 CGTTTGTGACTGCAAGACTAGAGTCGTCAGAGGGGGTAGAATTCACCGTGTAGCAGTG 660
Qy 684 AAATGCGTAGAGTCCGAGGAATACCGTAGCGGAAGCAGCCCGCTGGGATGACACTGA 743
Db 661 AAATGCGTAGAGTGTGGAGGAACACCGTAGCGGAAGCAGCCCGCTGGGCAATACTGA 720
Qy 744 CGCTCATGCAAGAGCGTGGGAGCAACAGGATTAAGATACCTGTGTAGTCCAGCGCCT 803
Db 721 CGCTCATGCAAGAGCGTGGGAGCAACAGGATTAAGATACCTGTGTAGTCCAGCGCCT 780
Qy 804 AAACGATGCTAAATAGCTGTGGT - GGGTTTGAATCTTGTGTAGCTAGCTAAACGCGTGA 861
Db 781 AAACGATGCTAAATAGCTGTGGTGGGTTTAAACCCATTAGTGGCGTAGCTAAACGCGTGA 840
Qy 862 AATTGACCGCTGGGAGTACGGCCGAAGGTAAACTCAAGGAATTGACGGGGACCC 921
Db 841 AGTTGACCGCTGGGAGTACGGCCGAAGGTAAACTCAAGGAATTGACGGGGACCC 900
Qy 922 GCACAAGCGGTGATGTGGATTAATTCATGCAACGCGAAAAACCTTACCTGCTCTT 981
Db 181 GGCCTCGCTATAGGGTGGCCGATGGCTGATTAGCTAGTTGGTGGGTAAGAGCCCTAC 240
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RESULT 7
US-10-029-397A-42
; Sequence 42 Application US/10029397A
; Publication No. US20030175709A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, GEORGE L.
; APPLICANT: WHITLEY, J. PENN
; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS
; FILE REFERENCE: AMBI.07GUS
; CURRENT APPLICATION NUMBER: US/10/029,397A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 1488
; TYPE: DNA
; ORGANISM: Burkholderia mallei
US-10-029-397A-42
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Query Match      80.6%; Score 1159.8; DB 7; Length 1488;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 1264; Conservative 1; Mismatches 149; Indels 5; Gaps 1;

Qy 22 AGATTGAACCGTGGCGGCATGCTTTTACATGCAAGTCGAACGGTAAACAGGGTCTTGCA 81
Db 1 AGATTGAACCGTGGCGGCATGCTTTTACATGCAAGTCGAACGGTAAACAGGGTCTTGCA 60
Qy 82 CCGCTGACGAGTCGCGAACGGGTGAGTAATCGCTCGGAATGTACCGTGTATATGGGGATA 141
Db 61 CTGTGGCGAGTGGTGAACGGGTGAGTAATACATCGCAATGTCTGTAGTGGGGATA 120
Qy 142 GCTCGGGAAGCGCGGATTAATACCGCATACCGCTTGAAGGGGAAAGCGGGGATCGAAA 201
Db 121 GCGCGGGAAGCGCGGATTAATACCGCATACCGCTTGAAGGGGAAAGCGGGGATCG 180
Qy 202 GACCTCGGTTATACGAGCAGCGACGCTGATTAGCTAGTTGGTGAAGTGAAGCTCAC 261
Db 181 GGCCTCGCTATAGGGTGGCCGATGGCTGATTAGCTAGTTGGTGGGTAAGAGCCCTAC 240
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QY 262 CAAGGCGACGATCAGTAGCGGGTCTGAGAGGATGATCCGCCACACTGGGACTGAGACACG 321
Db 241 CAAGGCGACGATCAGTAGCTGTCTGAGAGGACGACGACGACCACTGGGACTGAGACACG 300
QY 322 GCCAGACTCTCTACGGAGGAGCAGCAGTGGGGAATTTTGGACAATGGGGGCAACCTGTATC 381
Db 301 GCCAGACTCTCTACGGAGGAGCAGCAGTGGGGAATTTTGGACAATGGGGGCAACCTGTATC 360
QY 382 CAGCATGCCCGTGTCTGAAGAAGGCTTTCGGSTTGTAAAGACTTTTCTCAGGGAGGA 441
Db 361 CAGCAATGCCCGTGTGTGAAGAAGGCTTTCGGSTTGTAAAGACTTTTCTCAGGAAGA 420
QY 442 AATCCCGCTGTAAATACCCGGGGGATCACAGTACCBGAAGAATAAGCACCGGCTAAC 501
Db 421 AATCATTTCTGGCTAATACCCGGAGTGATGACGTACCGGAAGAATAAGCACCGGCTAAC 480
QY 502 TAGTGCACGACGCGCGGTAAATAGTAGGTGACAGCGTTAATCGGAATTAATCTGGCGGT 561
Db 481 TAGTGCACGACGCGCGGTAAATAGTAGGTGACAGCGTTAATCGGAATTAATCTGGCGGT 540
QY 562 AAAGCGTCCGAGCGGTTTGCAGTCTGATGTGAAGCCCGGGCTCAACCTGGGAAC 621
Db 541 AAAGCGTCCGAGCGGTTTGTGAACCGATGTGAATCCCGGGCTCAACCTGGGAAC 600
QY 622 GGCAATTGGAGACTGCAAGACTAGAGTGCCTCAGAGGGGGGTAGAATTTCCGCGTGTAGCAG 681
Db 601 TGCATTGGTCACTGGCAGGCTAGATGATGCGAGAGGGGGGTAGATTTCCACGTTAGCAG 660
QY 682 TGAATGCGTAGAGATCGGAGGAATACCGATGCGAGGACGCGCCCTGGGATGACACT 741
Db 661 TGAATGCGTAGAGATGCGAGGAATACCGATGCGAGGACGCGCCCTGGGCAATACT 720
QY 742 GACGCTCATCGCAAGCGTGGGAGCAACAGGATTAGATACCTGGTAGTCCACGCC 801
Db 721 GACGCTCATCGCAAGCGTGGGAGCAACAGGATTAGATACCTGGTAGTCCACGCC 780
QY 802 CTAAACGATGCAATTAGCTGTTGGGGGTTTGAATCCTGTTAGCGGTAGTAAACGGGTGA 861
Db 781 CTAAACGATGCAATTAGCTGTTGGGGATTCATTTCTTAGTAAACGTTAGCTAACCGGTGA 840
QY 862 AATTGACCGCTGGGAGTAGCGCGGCAAGGTTTAAACTCAAAAGGAATTTGACGGGACCC 921
Db 841 AGTTGACCGCTGGGAGTAGCGGTGCGCAAGTTTAAACTCAAAAGGAATTTGACGGGACCC 900
QY 922 GCACAAGCGTGGATGATGTGGATTAATTCGATGCAACGCGAAGAACTTTACCTGCTCTT 981
Db 901 GCACAAGCGTGGATGATGTGGATTAATTCGATGCAACGCGAAGAACTTTACCTACCTT 960
QY 982 GACATGTACGGAACCTTGGTAGAGATATCTTGGTGCCCGAAGGGAGCGGTAAACACAGGTG 1041
Db 961 GACATGTGCGAAGCGCGATGAGAGTTGGGCGTGCTCGAAGAGAACCGCGCGCACAGGTG 1020
QY 1042 CTCATGCGCTGCTGCTAGCTGCTGTGTGAGATGTTGGGTTAAGTCCCGCAACGACGGCA 1101
Db 1021 CTCATGCGCTGCTGCTAGCTGCTGTGTGAGATGTTGGGTTAAGTCCCGCAACGACGGCA 1080
QY 1102 ACCCTTGTCAATTAGTTGCCATATTTAGTTGGGCATCTTAATCAGACTGCGGTTGACAA 1161
Db 1081 ACCCTTGTCTTAGTTGCTACCGAAG-----GCATCTTAAGGAGACTGCGGTTGACAA 1135
QY 1162 CCGGAGGAAGGTGGGATGACGTCAAGTCTCATGCGCCCTTATGAGCAGGGCTTTCACAG 1221
Db 1136 CCGGAGGAAGGTGGGATGACGTCAAGTCTCATGCGCCCTTATGAGTGGGTTCACAG 1195
QY 1222 TCATACATGGTTCGGTACAGAGGTCGTAAGCCGCGAGGTGTGTCGAATCTCATAAAAC 1281
Db 1196 TCATACATGGTTCGGAAACAGAGGTCGCAACCCCGGAGGGGAGGCAATCCCAAGAAAC 1255
QY 1282 CGATCGTAGTCCGATCGCACTCTGCAACTCGAGTCGAGTGAAGTTCGGAATTCGCTAGTAA 1341
Db 1256 CGATCGTAGTCCGATTCGCACTCTGCAACTCGAGTCGAGTGAAGTTCGGAATTCGCTAGTAA 1315
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QY 1342 CGCAGATCAGCATCTGCGGTGAATACGTTCCCGGTCTTGTACACACCCCGCTCACAC 1401
Db 1316 CGCGGATCAGCATCGCCGCGGTGAATACGTTCCCGGTCTTGTACACACCCCGCTCACAC 1375
QY 1402 CATGGAGTGAAGTTTCCACGAAGTGGGTAGGCTAACCG 1440
Db 1376 CATGGAGTGGGTTTTTACCAGAAGTGGCTAGTCTAACCG 1414

RESULT 8
US-10-168-337A-2
; Sequence 2, Application US/10168337A
; Publication No. US20030170654A1
; GENERAL INFORMATION:
; APPLICANT: Crocetti, Gregory R.; Tyson, Gene W.; Hugenholtz, Philip; and Blackall,
; APPLICANT: Linda L.
; TITLE OF INVENTION: Probes and Primers for the Detection of Polyphosphate
; FILE REFERENCE: Accumulating Organisms in Wastewater
; FILE REFERENCE: 002367PC/KF
; CURRENT APPLICATION NUMBER: US/10/168,337A
; CURRENT FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Rhodocyclus tenuis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 50..59
; OTHER INFORMATION: n = unknown
US-10-168-337A-2
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Query Match      80.5%; Score 1159; DB 7; Length 1460;
Best Local Similarity 88.9%; Pred. No. 0;
Matches 1262; Conservative 1; Mismatches 154; Indels 2; Gaps 1;
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QY 24 ATTGAACGCTGGCGGATGCTTTACACATGCAAGTCCAAACGGTAAACAGGGTGTCTTGACC 83
Db 1 ATTGAACGCTGGCGGATGCTTTACACATGCAAGTCCAAACGGTAAACAGGGTGTCTTGACC 60
QY 84 GTGACGAGTGGCGAAACGGGTGAGTAAATCGCTCGGAATGTACCGTGTAAATGGGGATAGC 143
Db 61 GCGACGAGTGGCGAAACGGGTGAGTAAATCGATCGGAACGTGCCCTGAAAGTGGGGATAAC 120
QY 144 TCGGCGAAAGCCGATTAATACGATACGCTGAGGGGAAAGCGGGGATCGAAGA 203
Db 121 GTAGCGAAAGTTACGCTAATACCGCATATTTCTGTGAGCAGGAAGCAGGGGATCTTAGGA 180
QY 204 CCTCGCGTTATACGAGCAGCCGACGCTCTGATTAGCTTAGTTGGTGAAGTAAAGCTCACCA 263
Db 181 CCTTGGCTTTGGGAGCGGCCGATGTCGGATTAGCTTAGTTGGTGAAGTAAAGCTCACCA 240
QY 264 AGCGACGATCAGTAGCGGGTCTGAGAGATGATCCGCCACACTGGGACTGAGACACGGC 323
Db 241 AGCGACGATCAGTAGCGGGTCTGAGAGATGATCCGCCACACTGGGACTGAGACACGGC 300
QY 324 CCAGACTCTACGGGAGGAGCAGTGGGGAATTTTGGACAATGGGGGCAACCTGTATCCA 383
Db 301 CCAGACTCTACGGGAGGAGCAGTGGGGAATTTTGGACAATGGGGGCAACCTGTATCCA 360
QY 384 GCCATGCCCGTGTCTGAAGAAGGCTTTCGGGTGTGAAGAGCTTTTGTTCAGGAGGAAA 443
Db 361 GCCATGCCCGTGTGAAGAAGGCTTTCGGGTGTGAAGAGCTTTTTCGGGAGGAGAAA 420
QY 444 TCCCGCTGTTTAATACCCCGGGGATGACAGTACCBGAAGAATAAGCACCGGCTAACTA 503
Db 421 TGGCACTGGCTAATACCTGCTGATGACGGTACCCGAAGAAGAAGCACCGGCTAACTA 480
QY 504 CGTGCCAGCAGCCGGGTAAATACGTAGGTCGCAAGGTTAATCGGAATTTACTGGGCGTAA 563
Db 481 CGTGCCAGCAGCCGGGTAAATACGTAGGTCGAGCGTTAATCGGAATTTACTGGGCGTAA 540
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Qy 564 AGCGTCGCGAGCGGTTTTCGAAGTCTGATGCTGAAGCCCGCGGCTCAACCTCGGAACGG 623
Db |||||
Qy 541 AGCGTCGCGAGCGGTTGTGTAAGACAGAGCTGAATCCCGGGCTCAACCTGGGAACGTG 600
Db |||||
Qy 624 CATTGGAGACTGCAAGACTAGAGTCGCTCAGAGGGGGGTAGAATTCCCGCTGTAGCAGTG 683
Db |||||
Qy 601 CGTTTGTGACTGACACGCTAGAGTTTGGCAGAGGGGGTGGAAATTCACGCTGTAGCAGTG 660
Db |||||
Qy 684 AATGCGTAGAGATGCGGAGGAATACCGATGCGGGAAGCGAGCCCGCTTGGGATGACACTGA 743
Db |||||
Qy 661 AATGCGTAGAGATGTGGAGGAACACCGATGCGGGAAGCGAGCCCGCTTGGGCAATATCTGA 720
Db |||||
Qy 744 CGCTCATGCAAGAAAGCGTGGGAGCAACAGGAATTAGATACCTGTGTAGTCCACGCGCT 803
Db |||||
Qy 721 CGCTCATGCAAGAAAGCGTGGGAGCAACAGGAATTAGATACCTGTGTAGTCCACGCGCT 780
Db |||||
Qy 804 AAACGATGTCAATTAGCTGTGG--GGGGTTTGAATCTTGGTAGCTAGCTTAACGCGTGA 861
Db |||||
Qy 781 AAACGATGTCACTAGGTGTGGTGGGTAAACCCATTAGTGCCTAGCTTAACGCGTGA 840
Db |||||
Qy 862 AATTGACCGCTCGGGAGTACGGCCGCAAGGTTAAACTCAAGGAATTGACGGGACCC 921
Db |||||
Qy 841 AGTTGACCGCTCGGGAGTACGGCCGCAAGGTTAAACTCAAGGAATTGACGGGACCC 900
Db |||||
Qy 922 GCACAAGCGGTGATGTGGATTAAATTCGATGCAACGGGAACCTTACCTGCTCTT 981
Db |||||
Qy 901 GCAACAAGCGGTGATGTGGATTAAATTCGATGCAACGGGAACCTTACCTGCTCTT 960
Db |||||
Qy 982 GACATGTACGGAACTTGGTAGAGATATCTTGGTCCCGAAAGGAGCGGTAAACACAGGTG 1041
Db |||||
Qy 961 GACATGTACGGAACTTGGTAGAGATATGGGAGTCCCGAAAGGAACTTGAACACAGGTG 1020
Db |||||
Qy 1042 CTGATGCGCTGCTGCTAGCTGCTGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA 1101
Db |||||
Qy 1021 CTGATGCGCTGCTGCTAGCTGCTGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA 1080
Db |||||
Qy 1102 ACCCTGTGATTAGTGTGCATCTTATTGTTGGGCACTCTAATGAGACTGCCGGTGAACAA 1161
Db |||||
Qy 1081 ACCCTGTGATTAAATGTCATCTTATTGTTGGGCACTCTAATGAGACTGCCGGTGAACAA 1140
Db |||||
Qy 1162 CCGGAGGAAGTGGGGATGAGCTCAAGTCTCTCATGGCCCTTATGAGCAGGCTTCACACG 1221
Db |||||
Qy 1141 CCGGAGGAAGTGGGGATGAGCTCAAGTCTCTCATGGCCCTTATGGTAGGGCTTCACACG 1200
Db |||||
Qy 1222 TCATACAAATGTCGGTACAGAGGTGCTAGCCGCGAGGTTGGTCCCAATCTCATAAAC 1281
Db |||||
Qy 1201 TCATACAAATGTCGGTCCAGAGGTTGCCAACCCGCGAGGGGAGCCAATCCCGCAAGC 1260
Db |||||
Qy 1282 CGATCGTAGTCCGGATCGCACTCTGCAACTCGAGTGGTGAAGTCCGAATCGCTAGTAAT 1341
Db |||||
Qy 1261 CGATCGTAGTCCGGATGCACTCTGCAACTCGATGCAATGCAATGCAATGCAATGCAAT 1320
Db |||||
Qy 1342 CGCAGATCAGCATGTCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCAAC 1401
Db |||||
Qy 1321 CGCGGATCAGCATGTCGGGTTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCAAC 1380
Db |||||
Qy 1402 CATGGAGTAGTTTACCAAGTAGGTTAGGCTTAACCG 1440
Db |||||
Qy 1381 CATGGAGCGGGTTCTGCGAAGTAGTTAGCCTTAACCG 1419
Db |||||
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RESULT 9

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US-10-029-397A-45
; Sequence 45, Application US/10029397A
; Publication No. US20030175709A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, GEORGE L.
; APPLICANT: WHITLEY, J. PENN
; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS
; FILE REFERENCE: AMBI:076US
; CURRENT APPLICATION NUMBER: US/10/029.397A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 73
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 1544
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
US-10-029-397A-45
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Query Match 80.5%; Score 1159; DB 7; Length 1544;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 1286; Conservative 1; Mismatches 147; Indels 9; Gaps 3;
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Qy 4 AGAGTTTGTATCTTCGGCTCAGATTGAACGCTGGGGCATGCTTTACACATCAAGTCSAAC 63
Db |||||
Qy 9 AGAGTTTGTATCTTCGGCTCAGATTGAACGCTGGGGCATGCTTTACACATCAAGTCSAAC 68
Db |||||
Qy 64 GGTA-----ACAGGTGCTTTCACCGCTGACGAGTGGCGAAACGGGTGAGTAATGCCGTCG 117
Db |||||
Qy 69 GGCAGCACAGAGAAGCTTGTCTTCGGGTGGCGAGTGGCGAACGGGTGAGTAACATATCG 128
Db |||||
Qy 118 GAATGTACCGTGTAAATGGGGGATAGCTCGCGGAAAGCCGATTAAATACCGCATACGCCCT 177
Db |||||
Qy 129 GAACGTACCCGAGTAGTGGGGATAACTGATCGAAAGATCAGCTAATACCGCATACGCTT 188
Db |||||
Qy 178 GAGGGGAAAGCGGGGATCGAAAGACCTCGCGTTATACGAGCAGCCGACGCTCTGATTAG 237
Db |||||
Qy 189 GAGAGAGAAAGCAGGGGACCTTCGGGCTTTCGCTATTTCGAGCGCGCATATCTGATTAG 248
Db |||||
Qy 238 CTAGTTGGTGAAGTAAGAGCTACCAAGGCGAGCATAGTAGGGGTCTGAGAGGATGAT 297
Db |||||
Qy 249 CTAGTTGGTGGGTAAAGGCTTACCAAGGCGAGCATCAGTAGCGGCTCTGAGAGGATGAT 308
Db |||||
Qy 298 CCGCCACACTGGGACTGAGACACGGCCAGACTCTTACGGGAGGACAGCAGTGGGGAATTT 357
Db |||||
Qy 309 CCGCCACACTGGGACTGAGACACGGCCAGACTCTTACGGGAGGACAGCAGTGGGGAATTT 368
Db |||||
Qy 358 TGACAAATGGGGCAACCTTGATCCAGCCTATGCCGCTGTCTGAAGAAGCGCTTCGGGTT 417
Db |||||
Qy 369 TGACAAATGGGCGCAAGCCTGATCCAGCCTATGCCGCTGTCTGAAGAAGCGCTTCGGGTT 428
Db |||||
Qy 418 GTAAAGGACTTTTGTGAGGAGGAATCCGCTGTTTAATACCCGGGGGATGACAGTA 477
Db |||||
Qy 429 GTAAAGGACTTTTGTGAGGAGGAATCCGCTGTTTGTCTAATATCAGCGGCTGATACCGTA 488
Db |||||
Qy 478 CCBGAAGAATAAGCACCGGCTAACTAGCTGCAGCAGCCGCGTAAATACGTAGGCTGCAA 537
Db |||||
Qy 489 CTTGAAGAAATAGCACCGGCTAACTAGCTGCAGCAGCCGCGTAAATACGTAGGCTGCGA 548
Db |||||
Qy 538 GCGTTAATCGGAATTAATCGGCGTAAAGCGTGGCGAGCGGTTTTCGAAGTCTCATGTGA 597
Db |||||
Qy 549 GCGTTAATCGGAATTAATCGGCGTAAAGCGGCGCAGACGCTTACTTTAAGCAGGATGTGA 608
Db |||||
Qy 598 AAGCCCGGGCTCAACCTGGGAACGGCAATTGGAGACTGCAAGACTAGAGTCGCTCAGAGG 657
Db |||||
Qy 609 AATCCCGGGCTCAACCTGGGAACGGCAATTGGAGACTGCAAGACTAGAGTCGCTCAGAGG 668
Db |||||
Qy 658 GGGGTAGAAATCCGCGTGTAGCAGTGAATGCGTAGAGATGCGGAGGAATACCGATGGCG 717
Db |||||
Qy 669 GAGTAGAATTCACGTTGAGCAGTGAATGCGTAGAGATGAGGAGATACCGATGGCG 728
Db |||||
Qy 718 AAGCAGCCCTCTGGGATGACACTGACGCTCATGCAAGAAAGCGTGGGAGCAACAGGA 777
Db |||||
Qy 729 AAGCAGCCCTCTGGGACAACTGACGCTTATGCCCGGAAGCGTGGGTGAGCAACAGGA 788
Db |||||
Qy 778 TTAGATACCTGTTAGTCCACGCCCTAAACGATGCTCAATTAGCTGTTGGG--GGTTTGAAT 836
Db |||||
Qy 789 TTAGATACCTGTTAGTCCACGCCCTAAACGATGCTCAATTAGCTGTTGGGCAACCTGATT 848
Db |||||
Qy 837 CTTGGTAGCGTAGCTAAACGCGTGAATTTGACCCCTCGGGAGTACGCCGCCCAAGGTTAA 896
Db |||||
Qy 849 GCTTGGTAGCGTAGCTAAACGCGTGAATTTGACCCCTCGGGAGTACCGTTCGCAAGATTAA 908
Db |||||
Qy 897 AACTCAAAGGAATTGACGGGAGCCCGCAAGCGGTGATGATGTGAATTAATTCGATGC 956
Db |||||
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Db	1699362	AACGCGAAGAACCTTACCTGGTCTTGACATGTACGGAA--TCCTCCGGAGACAGGAGAGT	1699905
Qy	1017	CCGAAAGGGAGCCGTAAACACAGAGTGTCTGATGGCTGTCGTGAGTGTGAGATGT	1076
Db	1699904	GCCTTCGGGAGCCGTAAACACAGTGTCTGATGGCTGTCGTGAGTGTGAGATGT	1699845
Qy	1077	TGGTTAAAGTCCCGCAACGAGCGCAACCCCTGTGTCATTAGTTGCCATCATTTAGTTGGGCA	1136
Db	1699844	TGGGTTAAAGTCCCGCAACGAGCGCAACCCCTGTGTCATTAGTTGCCATCATTTAGTTGGGCA	1699785
Qy	1137	CTCTAATGACACTGCCGGTGACAAACGGAGGAGGTGGGGATGACGTCAAGTCTCTCATG	1196
Db	1699784	CTCTAATGACACTGCCGGTGACAAACGGAGGAGGTGGGGATGACGTCAAGTCTCTCATG	1699725
Qy	1197	GCCTTTATGAGCGGGCTTCACACGTCAATCAATGGTCGCTACAGAGGGTCGCTAAGCCG	1256
Db	1699724	GCCTTTATGAGCGGGCTTCACACGTCAATCAATGGTCGCTACAGAGGGTAGCCAGCCG	1699665
Qy	1257	CGAGGTGGTGCCCAATCTCAATAAACCGATCGTAGTCCGGATCGACTCTGCAACTCGAGT	1316
Db	1699664	CGAGGCGGAGCCAATCTCAATAAACCGATCGTAGTCCGGATTCGACTCTGCAACTCGAGT	1699605
Qy	1317	GCCTGAAGTCCGAATCGCTAGTAAATCCAGATCAGCATGCTGCGTGAATACGTTCCCGG	1376
Db	1699604	GCATGAAGTCGGAATCGCTAGTAAATCCAGGTGAGCATGCTGCGTGAATACGTTCCCGG	1699545
Qy	1377	GTCTTTGACACACGCGCCGTCACACATGGGAGTGAAGTTTCCACAGAAAGTGGGTAGGCTA	1436
Db	1699544	GTCTTTGACACACGCGCCGTCACACATGGGAGTGGGGGATACCAAGTAGGTAGGATTA	1699485
Qy	1437	ACC 1439	
Db	1699484	ACC 1699482	
RESULT 12			
US-10-168-337A-1			
; Sequence 1, Application US/10168337A			
; Publication No. US20030170654A1			
; GENERAL INFORMATION:			
; APPLICANT: Crocetti, Gregory R.; Tyson, Gene W.; Hugenholtz, Philip; and Blackall,			
; APPLICANT: Linda L.			
; TITLE OF INVENTION: Probes and Primers for the Detection of Polyphosphate			
; TITLE OF INVENTION: Accumulating Organisms in Wastewater			
; FILE REFERENCE: 002367PC/KF			
; CURRENT APPLICATION NUMBER: US/10/168,337A			
; CURRENT FILING DATE: 2000-12-27			
; NUMBER OF SEQ ID NOS: 14			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 1			
; LENGTH: 1460			
; TYPE: DNA			
; ORGANISM: Rhodocyclus tenuis			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: 50, 59, 881			
; OTHER INFORMATION: n = unknown, m = a or c			
US-10-168-337A-1			
Query Match 80.4%; Score 1157.6; DB 7; Length 1460;			
Best Local Similarity 88.8%; Pred. No. 0;			
Matches 1260; Conservative 2; Mismatches 155; Indels 2; Gaps 1;			
Qy	24	ATTGACGCTGGCGGATGTTTACATGCAAGTCGAAGTAAACAGGGTGTTCACC	83
Db	1	ATTGAAAGCTGGCGGATGCTTACATGCAAGTCGAAGTAAACAGGGGAAACCN	60
Qy	84	GCTGACGAGTGGCGAAGCGGTGAGTAAATGCGTGAATGACCGTGAATGGGGATAGC	143
Db	61	GGCGACGAGTGGCGAAGCGGTGAGTAAATGCAATGCGAAGTGCCTGNAAGTGGGGATAC	120
Qy	144	TCGGCGAAACCGGATTAATACCGCATACGCCCTGAGGGGGAAGCGGGGATCGAAGA	203

Db	121	GTAGCGAAAGTTACGCTAATAACCGCATATTTCTGTGACAGGAAGCAGGGGATCTTAGGA	180
Qy	204	CCTCGGTTTATACGACGACGCGACGCTCTGATTAGTAGTTGGTGAGGTAAAGACTCACCA	263
Db	181	CCTTGGCGTTTGGGACGCGCGGATGTCGGATTAGCTAGTTGGTGAGGTAAAGACTCACCA	240
Qy	264	AGCGACGATCAGTAGCGGGTCTGAGAGGATGATCCGCCACACTGGGACTGAGACACGGC	323
Db	241	AGCGACGATCAGTAGCGGGTCTGAGAGGATGATCCGCCACACTGGGACTGAGACACGGC	300
Qy	324	CCAGACTCCTACCGGAGGACAGTGGGAAATTTTGGACAAATGGGGCAACCTGTATCCA	383
Db	301	CCAGACTCCTACCGGAGGACAGTGGGAAATTTTGGACAAATGGGGGAAACCTGTATCCA	360
Qy	384	GCATGCCGCTGCTCTGAAGAAGGCTTCGGGTGTAAAGAGACTTTTGTTCAGGGAGGAAA	443
Db	361	GCATGCCGCTGAGTGAAGAAGGCTTCGGGTGTAAAGCTCTTTTCGGGGGGAAGAAA	420
Qy	444	TCCGCTGTGTTAATACCCCGCGGGGATGACAGTACCBGAAGAATAAGCACCGGCTAACTA	503
Db	421	TGGMACTGGCTAATACCTGCTGATGACGGTACCCGAAGAAGAAGCACCGGCTAACTA	480
Qy	504	CGTCCAGCAGCGCGCGTAACTAGTAGGGTGCAGCGTTAATCGGAATTAATCGGGCTAA	563
Db	481	CGTCCAGCAGCGCGCGTAACTAGTAGGGTGCAGCGTTAATCGGAATTAATCGGGCTAA	540
Qy	564	AGCGTCGCGAGCGGGTTCGCAAGTCTGATGTGAAAGCCCGGGCTCAACCTGGGAACGG	623
Db	541	AGCGTCGCGAGCGGGTTCGTAAGACAGACGTGAAATCCCGGGCTCAACCTGGGAACGT	600
Qy	624	CATTGGAGACTGCAAGACTAGAGTCGTGAGAGGGGGTAGAATTCGCGTGTAGCAGTG	683
Db	601	CGTTTGTGACTGCACAGCTAGAGTTTGGCAGAGGGGGTGAATTCACGCTGTAGCAGTG	660
Qy	684	AAATGCTAGAGATGCGGAGGAATACCGATGGCGAAGCGGCGCCCTGGGATGACACTGA	743
Db	661	AAATGCTAGAGATGCGGAGGAATACCGATGGCGAAGCGGCGCCCTGGGCGCAATACTGA	720
Qy	744	CGCTCATGCACGAAACGCTGGGAGCAAAACAGGATTAGATACCTGTGTAGTCCACGCGCT	803
Db	721	CGCTCATGCACGAAACGCTGGGAGCAAAACAGGATTAGATACCTGTGTAGTCCACGCGCT	780
Qy	804	AAACGATGTCAATTAGCTGTG--GGGGTTTGAATCCTTGGTAGCGGTAGCTAAACGCTGA	861
Db	781	AAACGATGTCAACTAGCTGTGTTGGTGGGTTTAAACCCATTAGTCCCGTAGCTAAACGCTGA	840
Qy	862	AATTGACCGCTGGGAGTACGCCCGCAAGGTTTAAAACTCAAAGGAATTGACGGGACCC	921
Db	841	AGTTGACCGCTGGGAGTACGCCCGCAAGGTTTAAAACTCAAAGGAATTGACGGGACCC	900
Qy	922	GCACAGCGGTGGATGATGTGGATTAAATTCGATGCAACGCGGAAACCTTACCTGCTCTT	981
Db	901	GCACAGCGGTGGATGATGTGGATTAAATTCGATGCAACGCGGAAACCTTACCTGCTCTT	960
Qy	982	GACATGTACGGAACTTTGGTAGAGATATCTTGGTCCCGGAAAGGAGCGGCTAAACAGGTG	1041
Db	961	GACATGTACGGAACTTTGGTAGAGATATCTTGGAGATGAGGAGTCCCGGAAAGGAACTTCA	1020
Qy	1042	CTGCATGGCTGTGTCAGCTGTCGTGAGATGTTGGGTAAAGTCCCGCAACAGGCGCA	1101
Db	1021	CTGCATGGCTGTGTCAGCTGTCGTGAGATGTTGGGTAAAGTCCCGCAACAGGCGCA	1080
Qy	1102	ACCTTGTCTATTAGTGGCATCATTTAGTTGGGCACTCTAACTCAGACTGCGCGTGACAAA	1161
Db	1081	ACCTTGTCTATTAGTGGCATCATTTAGTGGGCACTCTAACTCAGACTGCGCGTGACAAA	1140
Qy	1162	CCGGAGGAAGTGGGATGACGCTCAAGTCTCTCATGGCCCTTATGACAGGGCTTTCACAG	1221
Db	1141	CCGGAGGAAGTGGGATGACGCTCAAGTCTCTCATGGCCCTTATGAGGTAGGGCTTTCACAG	1200
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Db	1201	TCATCAATGGTGTGTGAGGGTTGCCAACCCCGGAGGGGAGGCAATCCCGCAAGC	1260


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; APPLICANT: WHITLEY, J. PENN
; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS
; FILE REFERENCE: AMB1:076US
; CURRENT APPLICATION NUMBER: US/10/029.397A
; PRIORITY FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 44
; LENGTH: 1544
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
; US-10-029-397A-44

Query Match      80.0%; Score 1152; DB 7; Length 1544;
Best Local Similarity 88.8%; Pred. No. 0;
Matches 1282; Conservative 1; Mismatches 152; Indels 9; Gaps 3;

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Qy 178 GAGGGGAAACCGGGGATCGAAGACCTCGCGTTATACGAGCGCGAGCTCTGATTAG 237
Db 189 GAGAGGAAACGAGGGGACCTTCGGGCTTTGCGCTATCCGAGCGCGCGATCTCTGATTAG 248

Qy 238 CTAGTTGCTGAGTAAGAGCTCACAAAGGCGACCATCAGTAGCGGGTCTGAGAGGATGAT 297
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Qy 298 CCGCCACACTGGGACTGAGACACCGCCAGACTCTTACGGGAGGCGAGCTGCGGGAATTT 357
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Qy 358 TGGCAATAGGGGCAACCCCTGATCAGCGCATGCGCGCTGTCTGAAGAAGCCCTTCGGGTT 417
Db 369 TGGCAATAGGGGCGCAAGCCCTGATCAGCGCATGCGCGCTGTCTGAAGAAGCCCTTCGGGTT 428

Qy 418 GTAAAGGACTTTTCTCAGGGAGGAATCCCGCTGTTTAATACCGCGGGGATGACAGTA 477
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Qy 478 CCBGAAGAATAAGCACCGGCTAACTACGTGCGCAGCAGCGCGGTAATACGTAGGGTGCAA 537
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Qy 538 CGGTAAATCGGAATTAAGTGGCGTAAAGCGTGGCGAGCGGTTTTCGAAGTCTGATGTA 597
Db 549 CGGTAAATCGGAATTAAGTGGCGTAAAGCGTGGCGAGCGGTTTTCGAAGTCTGATGTA 608

Qy 598 AAGCCCCGGGCTCAACTCTGGGAACCGCATGGAGACTGCAAGACTAGAGTGGCTCAGAGG 657
Db 609 AATCCCCGGGCTCAACCCGGGAATCGGTTCTGAACTGGGTGACTCGAGTGTGTCAGAGG 668

Qy 658 GGGGTAGAAATTCGCGGTGATGAGCAATGCGGTAGAGATGCGGAGGAATACCGATGGCG 717
Db 669 GAGGTGAAATTCACCGGTGATGAGCAATGCGGTAGAGATGCGGAGGAATACCGATGGCG 728

Qy 718 AAGCAGCCCCCTGGGATGACATGACGCTCATGCAGAAAGCGTGGGGAGCAACAGGA 777
Db 729 AAGCAGCCCCCTGGGATGACATGACGCTCATGCAGAAAGCGTGGGGAGCAACAGGA 788

Qy 778 TTAGATACCCCTGGTGGTCCAGCCCTAAACGATGCTCAATTAGCTGTGGG-GGTTTGAAT 836
Db 789 TTAGATACCCCTGGTGGTCCAGCCCTAAACGATGCTCAATTAGCTGTGGGCAACTTGAT 848
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Qy 897 AACTCAAGGAATTTAGCGGGGACCCGCAACGCGGTGGATGATGTGGATTAAATTCGATGC 956
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Db 1027 GCCTTCGGGAGCCGTAACACAGGTGCTGATGCGTGTGTCAGCTCGTGTGTCGAGATGT 1086

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; Sequence 5, Application US/10719633
; Publication No. US20040137485A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/10/719,633
; PRIORITY FILING DATE: 2003-11-21
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1544
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
; US-10-719-633-5

Query Match      80.0%; Score 1152; DB 8; Length 1544;
Best Local Similarity 88.8%; Pred. No. 0;
Matches 1282; Conservative 1; Mismatches 152; Indels 9; Gaps 3;

Qy 4 AGAGTTTGATCTCGCTCAGATTGAACCGCTGGCGGCATGCTTTACATGCAAGTCAAC 63
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Db 9 AGAGTTTATCTCGCTCAGATTGAACGCTGGCGCATGCTTTACATGCAAGTCGGAC 68
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Db 189 GAGAGGGAACGAGGGGACCTTCGGGCTTCGCGTATCCGAGCGCGCATATCTGATTAG 248
Qy 238 CTAGTTGTGAGGTAAAGACTCACCAAGGCGACGATCAGTAGCCGGTCTGAGAGGATGAT 297
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Db 1447 ACCG 1450

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Job time : 1998 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2006, 02:07:20 ; Search time 27 Seconds
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Perfect score: 1439.2

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 448628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	221.2	15.4	5849	7	US-11-270-287-1
3	125.4	8.7	1799	7	US-11-217-529-195588
4	125.4	8.7	1799	7	US-11-217-529-195589
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6	125.4	8.7	1799	7	US-11-217-529-195591
7	125.4	8.7	1799	7	US-11-217-529-195592
8	119.8	8.3	1773	7	US-11-256-428-61
9	103.2	7.2	22118	7	US-11-284-877-16
10	103	7.2	1869	6	US-10-511-937-333
11	91	6.3	42999	7	US-11-284-877-17
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13	40	2.8	600	7	US-11-217-529-166173
14	39.4	2.7	954	6	US-10-488-619-1
15	35	2.4	883	7	US-11-256-428-46
16	35	2.4	883	7	US-11-256-428-64
17	32.8	2.3	3228	6	US-10-342-836-47
18	28.8	2.0	378	7	US-11-284-877-22
19	28.6	2.0	2747	6	US-10-196-749-101
20	28.4	2.0	381	7	US-11-217-529-166773
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23	28	1.9	1389	7	US-11-217-529-78881
24	27.4	1.9	984	7	US-11-217-529-327
25	27.2	1.9	822	7	US-11-217-529-174437

ALIGNMENTS

RESULT 1

US-11-256-221-1

; Sequence 1, Application US/11256221

; Publication No. US20060094094A1

; GENERAL INFORMATION:

; APPLICANT: Sugio, Tsuyoshi

; APPLICANT: Miura, Akira

; APPLICANT: Parada Valdecantos, Pilar A.

; APPLICANT: Badilla Ohlbaum, Ricardo

; TITLE OF INVENTION: BACTERIA STRAIN WENELEN DSM 16786, USE OF SAID BACTERIA FOR

; TITLE OF INVENTION: LEACHING OF ORES OR CONCENTRATES CONTAINING METALLIC SULFIDE

; TITLE OF INVENTION: MINERAL SPECIES AND LEACHING PROCESSES BASED ON THE USE OF SAID

; FILE OF INVENTION: BACTERIA OR MIXTURES THAT CONTAIN SAID BACTERIA

; FILE REFERENCE: 15053.15US01

; CURRENT APPLICATION NUMBER: US/11/256, 221

; CURRENT FILING DATE: 2005-10-21

; PRIOR APPLICATION NUMBER: CL 2731-2004

; PRIOR FILING DATE: 2004-10-22

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1

; LENGTH: 1531

; TYPE: DNA

; ORGANISM: Bacteria

US-11-256-221-1

Query Match 71.5%; Score 1029.4; DB 7; Length 1531;

Best Local Similarity 83.5%; Pred. No. 0;

Matches 1203; Conservative 1; Mismatches 233; Indels 4; Gaps 3;

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Db 119 TCTGTCTTTTAGTGGGGGACCAACCCAGGGAACCTTGGGCTTAATACCGCATACCCCTTGAG 178

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Qy 241 GTTGGTGAGGTAAGAGCTACCAAGCGGACGATCAGTAGCGGCTCTGAGAGGATGATCCG 300

Db 241 GTTGGTGAGGTAAGAGCTACCAAGCGGACGATCAGTAGCGGCTCTGAGAGGATGATCCG 300

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Db 1319 ATGAAGTCGGAATCGCTAGTAAATCGCAGATCAGCATGCGCGGTGAATACGTTCCCGGCG 1378

Qy 1379 CTTGTACACACCGCCCGTCAACCATGGGAGTGAAGTTTACCAGAAAGTGGTAGGCTAAC 1438
Db 1379 CTTGTACACACCGCCCGTCAACCATGGGAGTGAAGTTTACCAGAAAGTGGTAGGCTAAC 1438
Qy 1439 C 1439
Db 1439 C 1439

RESULT 2

US-11-270-287-1
; Sequence 1, Application US/11270287
; Publication No. US20060099627A1
; GENERAL INFORMATION:
; APPLICANT: Kara, Anna K.
; APPLICANT: Ting, Robert C.
; APPLICANT: Tham, Jill M.
; APPLICANT: Nelson, James S.
; APPLICANT: Tan, Theresa M.
; TITLE OF INVENTION: Diagnosis of Parasites
; FILE REFERENCE: 64-99
; CURRENT APPLICATION NUMBER: US/11/270,287
; PRIOR FILING DATE: 2005-11-09
; PRIOR APPLICATION NUMBER: US/09/369,992
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: PCT/IB98/00212
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: AU P09481/97
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: AU P09329/97
; PRIOR FILING DATE: 1997-04-21
; PRIOR APPLICATION NUMBER: AU P04953/97
; PRIOR FILING DATE: 1997-02-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 5849
; TYPE: DNA
; ORGANISM: Plasmodium berghei
US-11-270-287-1

Query Match 15.4%; Score 221.2; DB 7; Length 5849;
Best Local Similarity 54.8%; Pred. No. 1.4e-64;
Matches 645; Conservative 0; Mismatches 468; Indels 63; Gaps 8;

Qy 229 TCTGATTAGCTAGTTGGTGAAGTCAACCAAGCGGACGATCAGTAGCGGGTCTGA 288
Db 4414 TTTGATTAACTAGTTGGTAAATAAAGCCCTACCAAGGTTATGATCAAAAATTCGTTTTA 4473
Qy 289 GAGGATGATCGCCACACT-GGGACTGAGACACGCGCCAGACTCTTACGGGAGGACGAG 347
Db 4474 AAGAAATGTACAATCACATTAGGGATTGAAATAAAGCCCTAAATTTTTTAAATCAGAG 4533
Qy 348 TGGGGAATTTTGGACAATGGGGCAACCTGATCCAGCCATGCGCGTGTCTGAAGAAG 407
Db 4534 TGAGAAATTTTACATGAGCGTAAGCTTGATAAGTAATATTTCTTAAAGGATGACAG 4593
Qy 408 CTTTCGGGTTGTAAAGACTTTTGTCAAGGAGGAAATCCCGCTGGTTAAATCCCGGGGG 467
Db 4594 TATATTTTATATTGTAACCTTTATA-----TTTTATTTTAAAT 4633
Qy 468 GATGACAGTACCBGAAGNATAAGCAGCCGGCTAACTAGTCCAGCAGCGCGGTAATACG 527
Db 4634 ATTGATAAAAAATAAAACATTAGTATTTGCTTAATTTCTGTGCGCAGCAGCGGTAATACA 4693
Qy 528 TAGGTGCAACCGTTAATTCGGAATTTACTGGCGGTAAAGCGTCCGAGCGGTTTTCGAAG 587
Db 4694 GAAATAACCGGTTATTC-ACITTTATTTGCGTAAGCGTTTTTAAGGTTTTATATTAAT 4752
Qy 588 TCTGATGTGAAGCCCGGGCTCAACCTCGGGAACGGCATTTGGAGACTCAAGACTAGAGT 647
Db 4753 TTTATTTTAAATAATTTTAAATTTAAATTTGAAATAAAAAATAAATAATAATAAAGAGT 4812

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QY 648 GCCTCAGAGGGGGTAGAATTCGCGTGTAGCAATGAAATCGGTAGAGATCGCGAGGAAT 707
Db 4813 ATTATAAAGATTAATAAGAAATTTTGGAGAGTAGTGAATGCAATGATACAAAAGAAAT 4872
QY 708 ACCGATGCGGAAGCAGCCGCCCTGGGATGACACTGACGCTCATGACGAAAGCGTGGGA 767
Db 4873 ACCAAGCGGAAGCATAAATACTATATAAATACTGACACTTATAAACGAAAGCTAAGGTA 4932
QY 768 GCAACAGGATTAGATACCTCGTGTAGTCCAGCGCCTAAACGATGCTCAATTAGCTGTGGG 827
Db 4933 GCAAAATAGGATAGATACCTTAGTGTCTTAGCTGTAAACTATGAATATTTATATTTAT 4992
QY 828 GGTTTGAATCCTTGGTAGCGTAGTAACGCGTGAATTTGACCGCTGGGGAGTACGCGCG 887
Db 4993 ATATT--AATATAAATAATAAATAAATAAATAATTTCCGCTGAGTAGTATATTCG 5050
QY 888 CAAGGTTAAACTCAAGGAATTTGACCGGGACCGGACCAAGCGGTGATGATGGAATTA 947
Db 5051 CAAGAACGAAATTCAAAGGAATTTGACGGGAGCTTTATCAAGTGGTGAACATGTGGCTTA 5110
QY 948 ATTCGATGCAACGGGAAACCTTTACCTGCTCTTGACATGTACGGAACCTTGGTAGATA 1007
Db 5111 ATTGATGCAACGATAAACCCTTACCATAATTTAACATAATTTTATTAATTAAGGAAT 5170
QY 1008 TCTTGTGCGCCGAAAGGGACCGGTAACACAGGTGCTGTCATGCTGGCTGCTGATCGTGC 1067
Db 5171 AATAGTTTAAATAAAA-----TATATAGGTAGTGCATGGCTGCTGCTGATCGTGC 5221
QY 1068 GTGAGATGTTGGGTTAAGTCCCGAACGAGCGGACCCCTTGTCTATTTAGTGGCCATAT 1127
Db 5222 GTGAAGTATTAATTTAAGTATTAACGAAACGTAACCCCTTTTATAAAAAAATTTTTAT 5281
QY 1128 AGTTGGGCACCTCTAATGAGACTGCGGTGACAAACGGGGAAGGTGGGGATGACGTC 1187
Db 5282 AATATATTTAATAAT-----ATATAAAGAACTACGTC 5318
QY 1188 GTCTCATGCGCCCTTATGACGAGGGCTTCACAGTGCATACAAATGCTCGGTACAGAGG 1247
Db 5319 GTCAATATGCTCCTTATATTTTGGGCTGCTCACGTGTACATAAATAATAACAATTTT 5378
QY 1248 GCTAAGCGCGAGGTGTCATTAATCAATAAACCGATCGTAGTCGGATCGCACTGTC 1307
Db 5379 ATTA-----TATGAAATAATAATAATAATAATAATAATAATAATAATAATAATA 5432
QY 1308 AACTCGAGTGCCTGAAGTTCGCTAGTAAATCGCAGATCAGCA-TGCTGCGGTGAAT 1366
Db 5433 AACTCATTTATGAAGATGGAATCACTAGTAAATCGCTAATAAAGATATAGCGGTGAAT 5492
QY 1367 ACCTTCCCGGCTTTGTACACACCGCCGTCACACC 1402
Db 5493 AAGTTCTTAAGCTTTGTACACACCGCCCGTCACATC 5528
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RESULT 3

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US-11-217-529-195588
; Sequence 195588, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
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; SEQ ID NO 195588
; LENGTH: 1799
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; US-11-217-529-195588
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Query Match 8.7%; Score 125.4; DB 7; Length 1799;
Best Local Similarity 54.8%; Pred. No. 1.4e-32;
Matches 438; Conservative 0; Mismatches 321; Indels 40; Gaps 8;
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QY 649 CGTCAGAGGGGGTAGAATTCGCGTGTAGCAATGAAATCGGTAGAGATCGCGAGGAATA 708
Db 869 CGTCCGGGGGCAATCAGTATTTCAATTTGTCAGAGGTGAAATTTCTTGGATTTATTGAAGACTA 928
QY 709 CCATCGGCAAGGACAGCCCTCGGATGACACTGACGCTCATGACGAAAGCGTGGGGAG 768
Db 929 ACTACTGCGAAGACATTTGCCAAGGACGTTTTCATTAACTCAAGAAAGATTAGGGGAT 988
QY 769 CAAACAGGATTAGATACCTGTGTGTCACCGCTTAAACGATCTCAATTAGCTGTGGGG 828
Db 989 CGAAGATGATCAGATACCGTGTGTTAAACCATAACTATGCCGACTAGGATCGGGT 1048
QY 829 GTTTGAATCCTTGGTAGCGTAGCTAACGCGTGAATTTGACCGCT-----G 874
Db 1049 GGTGTTTTTAAATGACCCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGG 1108
QY 875 GGAGTACCGCGCAAGGTTTAAACTCAAAGGAATTTGACGG-GCACCCGCAAGCGGTG 933
Db 1109 GGAGTATGTCGCAAGGCTGAAACTTAAAGGAATTTGACGGAAGGCGACCAACGAGGTG 1168
QY 934 GATGATGTGGAATTAATTCGATGCAACCGGAAACCTTACCTGCTCTTGAATGTACGGA 993
Db 1169 GAGCTCTCGGCTTAAATTTGACTCAACACGCGGGAACCTCACAGGTCCAGACA-----C 1221
QY 994 ACTTGTGATAGATATCTTGTGTCGCCCAAGGAGCGGTAAACAGGTGCTGATGCTGT 1053
Db 1222 AATAAGGATTGACAGATGAGAGCTCTTTCTTGAATTTGTGGGTGTGTCATGCGCT 1281
QY 1054 CGTCAGCTCGTGTGAGATGTTGGGTTAAAGTCCCGCAACGAGCGCAACCTT----- 1106
Db 1282 TCTTGTGTTGGAGTGAATTTGCTGCTTAATTCGATTAACGAAACGAGACCTTAACCTAC 1341
QY 1107 TGTCAATTAGTGTGCATTTAGT-----TGCGCACTCTAATGAGACTGCCGTGACAAA 1161
Db 1342 TAAATAGTGTGTAGCAATTTGCTGTTATCCACTTCTTAGAGGGACTATCGGTTTCAAG 1401
QY 1162 CCGGAGGAGGTGGGATGACGTCAAGTCTCATGCGCCTT--ATGACGAGGCGTTCACA 1219
Db 1402 CGATGGAAGTTTGAGGCAATAACAGGTCTGTGATCCCTTAGACGTTCTTGGGCGCGACG 1461
QY 1220 CGTCATACAAATGGTACAGAGGTC---GCTAAGCGCGAGGTGGTGCCTCAATCTCAT 1276
Db 1462 CGCGCTACTGACGAGCGCAGGAGTCTAACTTGGCGGAGAGGTCTTGGTAACTTGT 1521
QY 1277 AAAAC-CGATCGTAGTCCGATCGCACTCTGCAACTCGAGTGGTGAAGTTCGAAATCGCT 1335
Db 1522 GAAATCCGCTGCTGCGGATAGAGCAATTTGTAATTTATTTGCTCTTCAACGAGGAATTCCT 1581
QY 1336 AGTAATCGCAGATCAGCATGCTCGGTGAATAGCTTCCCGGGTCTTGTACACACCGCCG 1395
Db 1582 AGTAAGCGCAAGTCAATCAGCTTGCCTTGTATTAGTCCCTTGTGTACACACCGCCG 1641
QY 1396 TCACACCATGGGAGTGAAT 1414
Db 1642 TCCTAGTACCGATGAAT 1660
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RESULT 4

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US-11-217-529-195589
; Sequence 195589, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
```



```
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 195589
; LENGTH: 1799
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-11-217-529-195589

Query Match      8.7%; Score 125.4; DB 7; Length 1799;
Best Local Similarity 54.8%; Pred. No. 1.4e-32;
Matches 438; Conservative 0; Mismatches 321; Indels 40; Gaps 8;

QY 649 CGTCAGAGGGGGTAGAATCCGCGGTGTAGCAGTGAATGCGTAGAGATCGGAGGATA 708
DB 869 CGGTGGGGGCATCAGTATTCAATTTGTTCAGAGGTGAATTTCTGGATTATTGAAGACTA 928

QY 709 CCGATGGCGAAGGAGCGCCCTGGGATGACACTGACGCTCATGCACGAAAGCGTGGGGAG 768
DB 929 ACTACTCGGAAGCATTTGCCAAGGACGTTTTCATTATCAAGAACGAAAGTTAGGGAT 988

QY 769 CAACAGAGATTAGATACCTCGGTAGTCCAGCCCTTAAACGATGTCATTAAGTCTGTTGGG 828
DB 989 CGAAGATGATCAGATACCGTGTAGTCTTAACCATTAATGCGGATAGGATCGGGT 1048

QY 829 GTTTGAATCCTTGGTAGGTAGTAAACGCGTGAATTTGACCGCCT-----G 874
DB 1049 GGTGTTTTTTTAATGACCCACTCGGCACCTTACGAGAAATCAAGTCTTTGGGTTCTGGG 1108

QY 875 GGGAGTACGGCCGCAAGGTTAAACTCAAAGGAATTGACGG-GGACCCGCAACAGCGGTG 933
DB 1109 GGGAGTATGTCGCAAGGCTGAACCTTAAAGGAATTTGACGGAAGGGACACCCAGGAGTG 1168

QY 934 GATGATGTGGAATTAATTCGATGCAACGCGAAGAAACCTTACCTGCTCTTGACATGTACGGA 993
DB 1169 GAGCCTGGGGCTTAATTTGACTCAACACGCGGGAACCTCACCAGGTCCAGACA-----C 1221

QY 994 ACTTGGTAGAGATATCTTGGTCCCGAAGGAGCGGTAAACACAGGTGCTGCATGGCTGT 1053
DB 1222 AATAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTTGTGGTGGTGCATGGCCGT 1281

QY 1054 COTCAGCTCGTGTCTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCTT----- 1106
DB 1282 TCTTAGTTGGTGGAGTATTGCTGCTTTAATTTGCGATAACGAAAGACCTTAACTTAC 1341

QY 1107 TGTCAATTAGTTCCTCAATTTAGT-----TGGGCACTCTAATGACACTGCCGGTGACAAA 1161
DB 1342 TAAATAGTGGTGTAGTATTCGCTTAAATTCGATTAATTCGATTAACGAGACCTTAACCTTAC 1401

QY 1162 CCGGAGGAAGGTGGGGATGACGTCAAGTCTCATGGCCCTT--ATGAGCAGGGCTTCACA 1219
DB 1402 CCGATGGAAGTTTGAGGCATTAACAGGTCTGTGATGCTTACAGCTTCTGGGCGCAG 1461

QY 1220 CGTCATACAAATCGCTGACAGAGGTC--GCTAAGCGCGAGGTGGTGCAATCTCAT 1276
DB 1462 CGCGCTACACTGACGAGCGCAGGAGTCTAAGCTTTGGCGGAGGCTTTGGTAATCTTGT 1521

QY 1277 AAAAC-CGATCTAGTCCGATCGCACTCTGCAACTCGAGTCCGTGAAGTCGGATCGCT 1335
DB 1522 GAAACTCCGCTGCTGGGGATAGAGCATTTGAAATTAATGCTCTTTCAACGAGGAATTCCT 1581

QY 1336 AGTAATCGCAGATCAGCATGCTGCGGTGAATACGTTCCCGGCTTTGTACACACCGCCCG 1395
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DB 1582 AGTAAGCGCAAGTCATCAGCTTGGTTGATTACGTCCCTGCTTTGTACACACCGCCCG 1641
QY 1396 TCACACCATGGGAGTGAGT 1414
DB 1642 TCGCTAGTACCGATTGAAT 1660

RESULT 5
US-11-217-529-195590
; Sequence 195590, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 195590
; LENGTH: 1799
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-11-217-529-195590

Query Match      8.7%; Score 125.4; DB 7; Length 1799;
Best Local Similarity 54.8%; Pred. No. 1.4e-32;
Matches 438; Conservative 0; Mismatches 321; Indels 40; Gaps 8;

QY 649 CGTCAGAGGGGGTAGAATTCGCGGTGTAGCAGTGAATGCGTAGAGATCGGAGGATA 708
DB 869 CGGTGGGGGCATCAGTATTCAATTTGTTCAGAGGTGAATTTCTGGATTATTGAAGACTA 928

QY 709 CCGATGGCGAAGGAGCGCCCTGGGATGACACTGACGCTCATGCACGAAAGCGTGGGGAG 768
DB 929 ACTACTCGGAAGCATTTGCCAAGGACGTTTTCATTATCAAGAACGAAAGTTAGGGAT 988

QY 769 CAACAGAGATTAGATACCTCGGTAGTCCAGCCCTTAAACGATGTCATTAAGTCTTGGG 828
DB 989 CGAAGATGATCAGATACCGTGTAGTCTTAACCATTAATGCGGATAGGATCGGGT 1048

QY 829 GTTTGAATCCTTGGTAGGTAGTAAACGCGTGAATTTGACCGCCT-----G 874
DB 1049 GGTGTTTTTTTAATGACCCACTCGGCACCTTACGAGAAATCAAGTCTTTGGGTTCTGGG 1108

QY 875 GGGAGTACGGCCGCAAGGTTAAACTCAAAGGAATTGACGG-GGACCCGCAACAGCGGTG 933
DB 1109 GGGAGTATGTCGCAAGGCTGAACCTTAAAGGAATTTGACGGAAGGGACACCCAGGAGTG 1168

QY 934 GATGATGTGGAATTAATTCGATGCAACGCGAAGAAACCTTACCTGCTCTTGACATGTACGGA 993
DB 1169 GAGCCTGGGGCTTAATTTGACTCAACACGCGGGAACCTCACCAGGTCCAGACA-----C 1221

QY 994 ACTTGGTAGAGATATCTTGGTCCCGAAGGAGCGGTAAACACAGGTGCTGCATGGCTGT 1053
DB 1222 AATAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTTGTGGTGGTGCATGGCCGT 1281

QY 1054 COTCAGCTCGTGTCTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCTT----- 1106
DB 1282 TCTTAGTTGGTGGAGTATTGCTGCTTTAATTTGCGATAACGAAAGACCTTAACTTAC 1341

QY 1107 TGTCAATTAGTTCCTCAATTTAGT-----TGGGCACTCTAATGACACTGCCGGTGACAAA 1161
DB 1342 TAAATAGTGGTGTAGTATTCGCTTAAATTCGATTAATTCGATTAACGAGACCTTAACCTTAC 1401

QY 1162 CCGGAGGAAGGTGGGGATGACGTCAAGTCTCATGGCCCTT--ATGAGCAGGGCTTCACA 1219
DB 1402 CCGATGGAAGTTTGAGGCATTAACAGGTCTGTGATGCTTACAGCTTCTGGGCGCAG 1461

QY 1220 CGTCATACAAATCGCTGACAGAGGTC--GCTAAGCGCGAGGTGGTGCAATCTCAT 1276
DB 1462 CGCGCTACACTGACGAGCGCAGGAGTCTAAGCTTTGGCGGAGGCTTTGGTAATCTTGT 1521

QY 1277 AAAAC-CGATCTAGTCCGATCGCACTCTGCAACTCGAGTCCGTGAAGTCGGATCGCT 1335
DB 1522 GAAACTCCGCTGCTGGGGATAGAGCATTTGAAATTAATGCTCTTTCAACGAGGAATTCCT 1581

QY 1336 AGTAATCGCAGATCAGCATGCTGCGGTGAATACGTTCCCGGCTTTGTACACACCGCCCG 1395
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Db 1402 CCATGGAAGTTTGGAGCAATAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCGGCACG 1461
Qy 1220 CGTCATAAATGGTTCGTACAGAGGGTC---GCTAAGCCGCGAGGTGGTCCCAATCTCAT 1276
Db 1462 CGCGCTACTAGCAGGAGCAGGAGTCAACCTTGGCCGAGAGGCTTGGTAATCTTGT 1521
Qy 1277 AAAC-CGATCGTAGTCCGGATCGCACTCTGCAACTCGAGTGGGTGAAGTCGGAATCGCT 1335
Db 1522 GAAATCCGTCTGGGATAGAGCATTTGTAATTATTCTCTTCAACGAGGAATTCCT 1581
Qy 1336 AGTAATCGAGATCAGATGCTCGGTGAATAGTTCCCGGGTCTTGTACACACCGCCG 1395
Db 1582 AGTAAGCGCAAGTCATCAGCTTGGTTGATTAGTCCCTCCCTTGTACACACCGCCG 1641
Qy 1396 TCACACCATGGGAGTGAGT 1414
Db 1642 TCCTAGTACCGATTGAAT 1660

RESULT 6

US-11-217-529-195591
; Sequence 195591, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 195591
; LENGTH: 1799
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-11-217-529-195591

Query Match 8.7%; Score 125.4; DB 7; Length 1799;
Best Local Similarity 54.8%; Pred. No. 1.4e-32;
Matches 438; Conservative 0; Mismatches 321; Indels 40; Gaps 8;
Qy 649 CGTCAGAGGGGGTAGAATTCGCGTGTAGCAGTGAATCGGTAGAGATCGGAGGAATA 708
Db 869 CGGTGGGGGCATCAGTATTCAATTGTACAGGTGAATTTCTGGATTATTGAAGACTA 928
Qy 709 CCATGCGGAAGGAGCGCCCTCGGTGATGACCTGATGACAGCTCATGACGAAGCGTGGGAG 768
Db 929 ACTACTGCGAAGCATTTGCAAGGACGTTTCAATTAATCAAGAAGCAAGATTAGGGAT 988
Qy 769 CAAACAGATTAGATACCTCGGTAGTCCACGCCCTAAACGATGTAATAGCTGTTGGG 828
Db 989 CGAAGATGATCAGATCCGTCGTAGTCTTAACCAATTAATCCGACCTAGGATCGGT 1048
Qy 829 GTTTGAATCTTGGTAGCTAGCTAAACGCGTGAATTTGACCGCT-----G 874
Db 1049 GGTGTTTTTTTAATGACCCACTCGGCACCTTACGAGAAATCAAGATCTTTGGTCTGGG 1108
Qy 875 GGAGTAGCGCCGAGGTTAAACTCAAGAGTAATGACGG--GGACCCGACAGCGGTG 933
Db 1109 GGGAGTATGTCGCAAGGCTGAACTTTAAAGAAATTGACGGAAGGGCACCACGAGGTG 1168
Qy 934 GATGATGCTGATTAAATTCGATGCAACGCGAAACCTTACCTCTTTGACATGTACGGA 993
Db 1169 GAGCTCGCGCTTAATTTGACTCAACACGGGGAATCTACCAGGTCCAGACA-----C 1221

Qy 994 ACTTGATAGAGATATCTCGTCCCGAAAGGAGCGGTAAACAGGTGCTGATGCTGT 1053
Db 1222 AATAAGATTGACAGATTGAGAGCTCTTTCTTGATTTTGTGGGTGGTGCATGGCCGT 1281
Qy 1054 CGTCAGCTCGTGTCTGAGATGTTGGTTAAGTCCCGCAACGAGCGCAACCTT----- 1106
Db 1282 TCTTAGTTGGTGGAGTGATTTGTCTGCTTAATTTGCGATAACGAACGAGACCTTAACTAC 1341
Qy 1107 TGTCAATTAGTTGCAATCAATTAGT-----TGGGCACTCTAATGAGACTGCCGTGACAA 1161
Db 1342 TAAATAGTGGTCTAGCATTTGCTGGTTATCACTTCTTAGAGGACTATCGTTTCAAG 1401
Qy 1162 CCGGAGGAAGTGGGATGACGTCAAGTCTCATGGCCCTT--ATGAGCAGGCGCTTACAC 1219
Db 1402 CCGATGGAAGTTTAGGCAATAACAGTCTGTGATGCCCTTAGACGTTCTGGGCGGCACG 1461
Qy 1220 CGTCATACATGGTCCGTACAGAGGTC---GCTAAGCCGCGAGGTGGTCCCAATCTCAT 1276
Db 1462 CGCGCTACACTGACGAGCCGAGGTCTAACCTTGGCCGAGAGGTCTTTGGTAACTTGT 1521
Qy 1277 AAAC-CGATCGTAGTCCGATCGCACTCTGCAACTCGAGTGGTGAAGTCGGAATCGCT 1335
Db 1522 GAAATCCGTCTGGTGGGATAGACATTGTAATTTATTTGCTCTTCAACGAGGAATTCCT 1581
Qy 1336 AGTAATCGCAGATCAGCATGCTCGGTGAATAGCTTCCCGGGTCTTGTACACACCGCCG 1395
Db 1582 AGTAAGCGCAAGTCATCAGCTTGGTTGATTAGTCCCTTGTGATACACACCGCCG 1641
Qy 1396 TCACACCATGGGAGTGAGT 1414
Db 1642 TCCTAGTACCGATTGAAT 1660

RESULT 7

US-11-217-529-195592
; Sequence 195592, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 195592
; LENGTH: 1799
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-11-217-529-195592

Query Match 8.7%; Score 125.4; DB 7; Length 1799;
Best Local Similarity 54.8%; Pred. No. 1.4e-32;
Matches 438; Conservative 0; Mismatches 321; Indels 40; Gaps 8;
Qy 649 CGTCAGAGGGGGTAGAATTCGCGTGTAGCAGTGAATTCGCGTGTAGAGATCGGAGGAATA 708
Db 869 CGGTGGGGGCATCAGTATTCAATTGTACAGGTGAATTTCTGGATTATTGAAGACTA 928
Qy 709 CCATGCGGAAGGAGCGCCCTCGGTGATGACCTGATGACAGCTCATGACGAAGCGTGGGAG 768
Db 929 ACTACTGCGAAGCATTTGCAAGGACGTTTCAATTAATCAAGAAGCAAGATTAGGGAT 988
Qy 769 CAAACAGATTAGATACCTCGGTAGTCCACGCCCTAAACGATGTAATAGCTGTTGGG 828
Db 989 CGAAGATGATCAGATACCGTCTGTAGTCTTAACCAATTAATCCGACCTAGGATCGGT 1048

QY 829 GTTGAATCCTTGTTAGTGGTACGTAACCGGTGAAATTTGACCGCCT-----G 874
Db 1049 GGTGTTTTTAAATGACCCACTCGGCACCTTTACGAGAAATCAAAAGTCTTTGGGTCTGGG 1108
QY 875 GGGAGTAGCGCGCAAGGTTAAACTCAAGAGAAATTCACGG-GGACCGGCACAGCGGTG 933
Db 1109 GGGAGTAGCGCGCAAGGCTGAAATTTAAAGAAATTTGACGAAGGACACACAGGAGTG 1168
QY 934 GATGATGTGGATTAAATTCGATGCAACCGGAAACCTTTACCTGCTCTTTGACATGTACGGA 993
Db 1169 GAGCTCGCGCTTAAATTTGACTCAACCGGGAACCTCACCGAGTCCAGACA-----C 1221
QY 994 ACTTGTTAGAGATATCTTTGGTCCCGGAAGGAGCGGTAAACAGGTGCTGCTGCTGCTG 1053
Db 1222 AATAAGGATTACAGATTTGAGAGCTCTTTCTTTGATTTTGTGGGTGGTGGTGCATGGCCGT 1281
QY 1054 CGTCAGCTCGTCTGAGATGTTGGGTAAAGTCCCGCAACGAGCGAACCT----- 1106
Db 1282 TCTTAGTTGGTGGAGTATTTGCTGCTTAATTTGGATAACAGACCTTTAACCTAC 1341
QY 1107 TGTCAATTAAGTTCATCATCTTTAGT-----TGGGCACCTCTAATGAGACTGCCGGTGACAAA 1161
Db 1342 TAAATAGTGGTGTAGCATTTGCTGGTTATCCACTTCTTAGAGGACTATCGGTTTCAAG 1401
QY 1162 CGGAGGAAGTGGGATGACGTCAAGTCTCATGCGCCCTT--ATGAGCAGGCTTACACA 1219
Db 1402 CCGATGGAAGTTTGAGGCAATAACAGGCTCTGTGATGCCCTTTAGACGTTCTGGGCGCGACG 1461
QY 1220 CGTCATCAATGTCGGTACAGAGGTC- -GCTAAGCGCGAGGTGGTGCAATCTCAT 1276
Db 1462 CGCGTACACTGACGGACCGAGCTAACCCTTGGCCGAGAGGTCTTGGTAATCTTGT 1521
QY 1277 AAAAC-CGATCGTAGTCCGATCGCACTCTCGCACTCGAGTGCCTGGAAGTCGGAATCGCT 1335
Db 1522 GAAACTCGTCTGCTGGGATAGAGCATTTGTAATTAATGCTCTTCAACGAGGAATCTCT 1581
QY 1336 AGTAATCCAGATCAGATGCTCGGTGAATACGTTCCGGGTCTTGTACACACGCGCG 1395
Db 1582 AGTAAGCGCAAGTCATCAGTTCGGTTGATTTACGTCCTGCTGCTTGTACACACGCGCG 1641
QY 1396 TCACACCATGGAGTGAGT 1414
Db 1642 TCGTAGTACCGATTGAAT 1660

RESULT 8

US-11-256-428-61
; Sequence 61, Application US/11256428
; Publication No. US20060095987A1
; GENERAL INFORMATION:
; APPLICANT: Niblett, Charles L.
; TITLE OF INVENTION: Methods and Materials for Conferring Resistance to Pests and
; TITLE OF INVENTION: Pathogens of Plants
; FILE REFERENCE: VEN-100
; CURRENT APPLICATION NUMBER: US/11/256,428
; CURRENT FILING DATE: 2005-10-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
; LENGTH: 1773
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Pratylenchus scribneri rdna
US-11-256-428-61

Query Match 8.3%; Score 119.8; DB 7; Length 1773;
Best Local Similarity 51.7%; Pred. No. 1.1e-30;
Matches 408; Conservative 4; Mismatches 341; Indels 36; Gaps 5;
QY 654 GAGGGGGGTAGAAATTCGCGGTGTCAGTGAATCGTAGAGATCGGAGGAATACCGAT 713

Db 855 GGGGGCATTCGTATTGCTACGTGAGAGTGAAATTTCTTGACCGTAGCAAGACGAACTAC 914
QY 714 GGGCAAGCGACCCCTGGGATGACACTGACGCTCATGACGAAAGCGTGGGAGCAAAAC 773
Db 915 AGCGAAGCAATTTGCCAAGAATGTCTTCAATTAACAAGAAATTCAGAGGTTCGAAG 974
QY 774 AGAATTAGATACCTGTTAGTACGCGCTTAAACGATGTCAATTTAGCTGTTGGGGTTTG 833
Db 975 GCGATCAGATACCGCCCTTGTCTTGACCGTAAACGATGCAACTAGCAKATCCCGCGGG 1034
QY 834 AATCCTTTGGTAGCGTAGCTAACCGGTGAAATTT-----GACCGCTGGGGAGTA 881
Db 1035 AATCTTGCCCTGGTGGGAGCTTCCCGGAAACGAAAGTCTTCCGGTTCCGGGGAAGTA 1094
QY 882 CGGCGCAAGGTTAAACTCAAGGAATTCACGG-GGACCGGCACAGCGGTGATGATG 940
Db 1095 TGGTTGCAAGCTGAACTTTAAAGGAATTCACGGAAGGACCACCAAGAGTGGAGCGCTG 1154
QY 941 TGGATTAAATTCGATGCAACCGGAAACCTTACTGCTCTTGCATGTACGGAACTTTGGT 1000
Db 1155 CGGCTTTAATTTGACTCAACGCGGAAACTCACCGGCCGGACACCGTAAGGATTGCA 1214
QY 1001 AGAGATATCTTTGGTGGCCGAAAGGAGCGGTAAACAGAGTGTCTGATGGTGTGTCAGC 1060
Db 1215 GATTTGATAGCTTTTTCATGATTCGGTG-----GATGGTGGTGCATGGCGCTTCTTAGT 1267
QY 1061 TCGTGTGCTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTT-----G 1108
Db 1268 TCGTGGAGCGAATTTGTCTGGYTTATTCGGATAACGAGCGAGACTCTGGCCTACTAAATAG 1327
QY 1109 TCATTAGTTCGCATCATTTTAGTTGGGCACCTTAATGAGACTGCCGTGACAAAACCGGAG 1168
Db 1328 TCGGCGCATTTGCTCTGTGTGCATGACTTCTTAGAGGGAATTTCCGTGTTTCAGCGCGACG 1387
QY 1169 AAGTGGGGTAGCGTCAAGTCTCTCATGGCCCTTATGACGAGGCTTTCACACGTCATACA 1228
Db 1388 AAATTTAGCAATAACAGGTCTGTGATGCCCTTAGATGTCCGGGGCTGCACGCGCTACA 1447
QY 1229 ATGTCGGTACAGAGGTTCGCTAAGCCGCGAGGTGG-----TGCCAACTCATATAAACCGA 1284
Db 1448 CTGCAAAATCAGCGTCTTGTCTCTCCGAAAGGAGTTGGTAAACCATTTGAAAAATTTG 1507
QY 1285 TCGTAGTCCGATCGCACTCTGCAACTCGAGTGGTGGTGAAGTCGGAATCGCTAGTAATCGC 1344
Db 1508 CCGTAGTTGGATCGGAAATTCGAATTAATTTTCGTGAAACGAGGAATTCGAAGTAAGTGC 1567
QY 1345 AGATCAGCATGCTCGGTGAATAGTTCGCGGTCTTTGTACACACCGCGCTCACCAT 1404
Db 1568 GAGTCATCAACTCGCGTTGATTACGTCCTGCCCTTTGTACACACCGCGCTCGCTGCC 1627
QY 1405 GGGAGTGAG 1413
Db 1628 GGGACTGAG 1636

RESULT 9

US-11-284-877-16
; Sequence 16, Application US/11284877
; Publication No. US20060095984A1
; GENERAL INFORMATION:
; APPLICANT: Hadlaczky, Gyula
; Szalay, Aladar
; TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND METHODS
; CORRESPONDENCE ADDRESS:
; STREET: 12390 El Camino Real
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92130
; COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA: US/11/284, 877
APPLICATION NUMBER: 10/808, 689
FILING DATE: 24-MAR-2004
APPLICATION NUMBER: 10/219, 694
FILING DATE: 14-AUG-2002
APPLICATION NUMBER: 10/151, 081
FILING DATE: 16-MAY-2002
APPLICATION NUMBER: 10/151, 078
FILING DATE: 16-MAY-2002
APPLICATION NUMBER: 10/125, 767
FILING DATE: 17-APR-2002
APPLICATION NUMBER: 10/287, 313
FILING DATE: 01-NOV-2002
APPLICATION NUMBER: 09/799, 462
FILING DATE: 05-MAR-2001
APPLICATION NUMBER: 09/724, 872
FILING DATE: 28-NOV-2000
APPLICATION NUMBER: 09/724, 726
FILING DATE: 28-NOV-2000
APPLICATION NUMBER: 09/724, 693
FILING DATE: 28-NOV-2000
APPLICATION NUMBER: 08/835, 682
FILING DATE: 10-APR-1997
APPLICATION NUMBER: 08/695, 191
FILING DATE: 07-AUG-1996
APPLICATION NUMBER: 08/682, 080
FILING DATE: 15-JUL-1996
APPLICATION NUMBER: 08/629, 822
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33, 779
REFERENCE/DOCKET NUMBER: 17084-004018/4020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-678-4777
TELEFAX: 202-626-7796
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-11-284-877-16

Query Match 7.2%; Score 103.2; DB 7; Length 22118;
Best Local Similarity 50.9%; Pred. No. 1.9e-24;
Matches 408; Conservative 0; Mismatches 348; Indels 46; Gaps 5;
QY 649 CGTCAGAGGGGGTAGAATTCGCCGTGTAGCAGTGAATCGCTAGAGATGCCGAGGAATA 708
Db 10570 CGCCCGGGGCATCTGTAATTCGCCCGCTAGAGTGAATCTTGGACCGCGCAAGACGG 10629
QY 709 CCGATGGCGAGGAGCCCGCTGGGATGACACTGACCTCATGCAGCAAGCGCTGGGGAG 768
Db 10630 ACCAGAGCGAAGCAATTTGCCAAGATGTTTCAATTAATCAAGAACGAAAGTCGAGGTT 10689
QY 769 CAACAGGATTAGATACCTCTGGTAGTCCAGCCCTAAACGATGCTAATAGCTGTTGGGG 828

Db 10690 CGAAGACGATCAGATACCGTCGTAGTTCGGAACCAATAAACGATCCGACATGGCGATCGGC 10749
QY 829 GTTTGAATCTTGGTAGCGTAGCTAACGGCGTGAATTTGACCG-----CCTG 874
Db 10750 GCGGTTATTCCTCATGACCCCGCGGAGCTTCGGGAAACCAAGTCTTTGGGTTCCGGG 10809
QY 875 GGGAGTACGGCCGCAAGGTTTAAAACTCAAAGGAATTTAGCGGGGACCCGACAAAGCGGTG 934
Db 10810 GGGAGTATGGTTGCAAAAGCTGAAACTTAAAGGAATTTACGGAAGGCGACCCACAGGAGTG 10869
QY 935 ATGATGTGATTAATTCGATGCAACCGGAAACCTTACCTGCTCTTGATCATGACGAA 994
Db 10870 GGCCTCGGCTTAATTTGACTCAACACGCGGAAACCTTACCCGCGCGGACACGACAGGA 10929
QY 995 CTTGGTAGAGATATCTTGGTCCCGGAAAGGAGCGCTAAACACAGGTGCTGATGGCTGTC 1054
Db 10930 TT-----GACAGATTGATGCTCTTCTCGATTCGGTGGTGGTGGTGCATGGCGTT 10982
QY 1055 GTCAGCTCGTGTGAGATGTTGGTTAAAGTCCGCAACGAGCGCAACCCCTTG----- 1108
Db 10983 CTTAGTTGGTGGAGCGATTTGCTGCTTAATTCGATAACGAACGAGACTCTCGCATGCT 11042
QY 1109 ----TCATTAGTTGCCATCAATTTAGTTGGGCACTC-----TAATGAGACTGCGGT 1155
Db 11043 AACTAGTTACGCGACCCCGAGCGGTGCGGCTCCCAACTTCTTAGAGGGAACAAGTGC 11102
QY 1156 GACAAACCGGAGGAGGTGGGATGACGTCAGTCTCATGGCCCTTATGAGCAGGCGTT 1215
Db 11103 GTTCAGCCACCGAGATTGAGCAATAACAGGCTCTGTGATGCCCTTAGATGTCGGGGCTG 11162
QY 1216 CACAGCTCATCAATGGTTCGGTACAGAGGGTTCGTAAGCGCGC-----AGGTGGTGCCA 1269
Db 11163 CAGCGCGCTACACTGACTGGCTCAGCGTGTGCTTACCTTCGCGCGGAGCGCGGTAA 11222
QY 1270 ATCTCAAAAACGATCGTAGTCCGATCGACTCTGCAACTCGAGTGGTGAAGTCGA 1329
Db 11223 CCCGTTGAACCCCAATTCGTGATGGGATCGGGATTCGCAATTTATCCCAATGAACGAGGA 11282
QY 1330 ATCGCTAGTAATCGCAGATCAGCATGCTCGGTGAATACGTTCCCGGGTCTTGTACACAC 1389
Db 11283 ATCCAGTAAGTGGGTCATAAGCTTGGTTGATTAAAGTCCCTGCCCTTTGTACACAC 11342
QY 1390 CGCCCGTCACACCATGGGAGTG 1411
Db 11343 CGCCCGTCGCTACTACCGATTG 11364
RESULT 10
US-10-511-937-333
; Sequence 333, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 50661200104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2

```
; SEQ ID NO 333
; LENGTH: 1869
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-333

Query Match          7.2%; Score 103; DB 6; Length 1869;
Best Local Similarity 52.4%; Pred. No. 5e-25;
Matches 421; Conservative 0; Mismatches 335; Indels 47; Gaps 7;

Qy 649 CGTCAGAGGGGGTAGAATCCCGCTGTAGCAGTGAATCGTAGAGATCGGAGGAATA 708
Db 927 CGGCGGGGGGATTCGTATTCCGCGCTAGAGGTGAATTCCTGGACGGGCGACAGCG 986
Qy 709 CCGATGGCGAAGGAGAGCCCTGGGATGACACTGACGCTCATGCACGAAAGCGTGGGGAG 768
Db 987 ACCAGAGCGAAGCATTTGCCAAGATGTTTCAATTAATCAAGAACGAAAGTCGGAGTT 1046
Qy 769 CAACAGGATTAGATACCTGTTAGTCCACGCCCTTAACGATGTCAATTAGCTGTTGGG 828
Db 1047 CGAAGACGATCAGATACCGTGTAGTTCGACCAATAAACGATGCCGCGCGATCGGC 1106
Qy 829 GTTTGAATCCTTGTAGCTAGCTAAGCGGTGAATTTGACCG-----CCTG 874
Db 1107 GCGGTTATCCCATGACCCGCGGGCAGCTTCCGGGAACCAAGTCTTTGGGTTCCGG 1166
Qy 875 GGGAGTAGCGCGCAAGGTTAAACTCAAAGGAATTAACCG-GGACCCGCAACAGCGGTG 933
Db 1167 GGGAGTAGTGGTTGCAAGCTGAAACTTAAGGAATTCACGGAAGGGCACCAAGGAGTG 1226
Qy 934 GATGATGGGATTAATTCGATGCAACGGAACCACTTACTGCTCTTTCATCATGACGGA 993
Db 1227 GAGCTCGGGCTTAATTTGACTCAACACGGGAACCTCACCCGCGCGGACACGACAGG 1286
Qy 994 ACTTGGTAGATATCTTGGTCCCGAAGGAGCGGTAACACAGGTGCTGCATGGCTGT 1053
Db 1287 ATT-----GACAGATTGATGCTCTTTCTCGATTCCGTGGTGGTGGTGCATGGCGT 1339
Qy 1054 CGTCAGCTCGTGTGCTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCTTGG----- 1108
Db 1340 TCTTAGTTGGTGGAGCGATTTGTCTGGTTAATTCGATTAACGAACGAGACTCTGGCATGC 1399
Qy 1109 ----TCATTAGTCCCATCAATTTAGTTGGGCACCTC-----TAATGAGACTGCCGG 1154
Db 1400 TAACTAGTTACGCGACCCCGAGCGGTGCGGCTCCGCCAACTCTTGAAGGGAACAAGTG 1459
Qy 1155 TGACAAACCGGAGGAGGTGGGATGACGTCAAGTCTCTCATGGCCCTTATGAGCAGGGCT 1214
Db 1460 CGTTCAGCCACCCGAGATTGAGCAATACAGGTCTGTGATGCCCTTAGATGTCGGGGCT 1519
Qy 1215 TCACAGCTCATCAATGTGCGGTACAGAGGT-----CGTTAAGCGCGGAGGTGGTGCCA 1269
Db 1520 GCACGCGCGTACACTGACTGCTGCTCAGCGTGTGCTTACCTACGCGCGGAGCGCGGTA 1579
Qy 1270 ATTCATAAACCGA--TCGTAGTCGGATCCGACTCTGCACTCGAGTGGCTGAAGTCGG 1328
Db 1580 ACCGTTGAACCCCACTCTCGTATGGGATCGGGATTGCAATTAATTCCTCCATGACAGG 1639
Qy 1329 AATCGTATGTAATCGCAGATCAGATGCTGGGGTGAATACGTTCCCGGGTCTTGTACACA 1388
Db 1640 AATTCACAGTAAGTGGGGTCAATAGCTTGGTTGATTAGTCCCTGCCCTTTGTACACA 1699
Qy 1389 CGGCCCGTCACACCATGGAGTG 1411
Db 1700 CGGCCCGTCTGCTACTACCGATTG 1722
```

RESULT 11

```
US-11-284-877-17
; Sequence 17, Application US/11284877
; Publication No. US20060095984A1
; GENERAL INFORMATION:
; APPLICANT: Hadlaczky, Gyula
```

```
; Szalay, Aladar
; TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND METHODS
; FOR PREPARING ARTIFICIAL CHROMOSOMES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 12390 El Camino Real
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92130
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/284,877
; FILING DATE: 21-Nov-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 10/808,689
; FILING DATE: 24-MAR-2004
; APPLICATION NUMBER: 10/219,694
; FILING DATE: 14-AUG-2002
; APPLICATION NUMBER: 10/151,081
; FILING DATE: 16-MAY-2002
; APPLICATION NUMBER: 10/151,078
; FILING DATE: 16-MAY-2002
; APPLICATION NUMBER: 10/125,767
; FILING DATE: 17-APR-2002
; APPLICATION NUMBER: 10/287,313
; FILING DATE: 01-NOV-2002
; APPLICATION NUMBER: 09/799,462
; FILING DATE: 05-MAR-2001
; APPLICATION NUMBER: 09/724,872
; FILING DATE: 28-NOV-2000
; APPLICATION NUMBER: 09/724,726
; FILING DATE: 28-NOV-2000
; APPLICATION NUMBER: 09/724,693
; FILING DATE: 28-NOV-2000
; APPLICATION NUMBER: 08/835,682
; FILING DATE: 10-APR-1997
; APPLICATION NUMBER: 08/695,191
; FILING DATE: 07-AUG-1996
; APPLICATION NUMBER: 08/682,080
; FILING DATE: 15-JUL-1996
; APPLICATION NUMBER: 08/629,822
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 17084-004018/402Q
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-678-4777
; TELEFAX: 202-626-7796
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42999 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-11-284-877-17

Query Match          6.3%; Score 91; DB 7; Length 42999;
Best Local Similarity 52.3%; Pred. No. 3.6e-20;
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Matches	421;	Conservative	0;	Mismatches	335;	Indels	49;	Gaps	8;
Qy	649	CGTCAGAGGGGGGTAGAAATTCGCGGTGTAGCAGTGAATAACGTAGAGATCGCGAGGAATA	708						
Db	4583	CGGCCGGGGGCATTTCGTATTTTCGGCCGTAGAGGTGAATAATCTTGGACCGGCGCAAGACGG	4642						
Qy	709	CCGATGCGGAAGCAGCCCGCTGGGTAGTGACACTGACGCTCATGCACGAAGACGTGGGGAG	768						
Db	4643	ACCAGCGGAAGCATTTGCCCAAGATGTTTTCAATTAATCAAGAACGAAAGTCGGAGGTT	4702						
Qy	769	CAAAACAGGATTAGATACCCCTGGTAGTCCACGCCCCATAACGATGTCAATTAGCTGTTCGGG	828						
Db	4703	CGAAGACGATCAGATACCGTCGTAGTTCCCGACCATAAACGATGCCGACCGCGATGCGGC	4762						
Qy	829	GTTTGAATCTTGGTGTAGGTAGCTAAACGCGTGAATTTGACCG-----CCTG	874						
Db	4763	GGCGTTATCCCATGAGCCCGCGGCGAGCTTTCGGGGAACCAAGATCTTTGGGTTCGGG	4822						
Qy	875	GGGAGTACGGCCGCAAGGTTAAAACTCAAAGGAATTCACGG-GGACCCGCACAAAGCGGTG	933						
Db	4823	GGGAGTATGGTTGCAAGAGCTCAAACTTTAAGGAATTCACGGAAGGGCACCAACAGAGATG	4882						
Qy	934	GATGATGTGGATTAAATTCGATGCAACCGCAAAAAACCTTACTGCTCTTGATCATGTACCGA	993						
Db	4883	GAGCCTCGGGCTTAATTTGACTCAACACGGGAAACCTCACCCGGCCCGGACACGACAGG	4942						
Qy	994	ACTTGGTAGAGATATCTTGGTGGCCGGAAGGGAGCCGTAACACAGGTGCTGCATGGCTGT	1053						
Db	4943	ATT-----GACAGATTGATAGCTCTTTCTCGAATCCGTGGGTGTGTCATGGCCGT	4995						
Qy	1054	CGTCAGCTCGTGTGCTGAGATGTTGGGTGTAAGTCCCGCAACGAGCGCAACCCCTTG-----	1108						
Db	4996	TCTTAGTTGGTGAGCGATTGTCTGTTAATTCGGATACGAACGAGACTCTGGCATGC	5055						
Qy	1109	-----TCATTAGTTGCCATCATTTAGTTGGGCATC-----TAATGAGACTGCCGG	1154						
Db	5056	TAACTAGTTACGCGACCCCGAGCGGTGCGCGTCCCCCAACTCTTTAGAGGGACAAGTGG	5115						
Qy	1155	TGACAAACCGGAGGAAGTGGGGATGACGTCAGTCTCATGCGCCCTTATGACGAGGCT	1214						
Db	5116	CGTTCAGCACCCGAGATTGAGCANATACAGGTCTGTGATGCCCTTAGATGTCCGGGCT	5175						
Qy	1215	TCACAGCTCATACAATGGTCCGTCACAGAGGT-----CGCTAAGCCGCGAGGTGGTGCCA	1269						
Db	5176	GCACGCGCGCTACACTGACTGGCTCAGCGTGTGCCTACCCTACGCGCGCAGGCGGGTA	5235						
Qy	1270	ATCTCATAAACCGA-TCGTTAGTCCGATCGCACTCTGCAACTCGAGTGGTGAAGTCGG	1328						
Db	5236	ACCCGTTGAACCCCATTCGTGTATGGGATCGGGATTCGCAATTAATCCCATGAAACGAGG	5295						
Qy	1329	AA--TCGCTAGTAATCCAGATCAGCATGCTGCGGTGAATACGTTCCCGGCTCTTGTACA	1386						
Db	5296	GAATCCCGAGTAAGTCGGGTATAGCTTGGTTGATTAAGTCTCGCCCTTGTACA	5355						
Qy	1387	CACGCCCGCTCACACCATGGAGTG	1411						
Db	5356	CACGCCCGCTCGCTACTACCGATTG	5380						

RESULT 12

RESULT 12
 US-11-217-529-166170
 ; Sequence 166170, Application US/11217529
 ; Publication No. US20060099612A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUNTORY LIMITED
 ; APPLICANT: NAKAO, YOSHIHIRO
 ; APPLICANT: NAKAMURA, NORIHIISA
 ; APPLICANT: KODAMA, YUKIKO
 ; APPLICANT: FUJIMURA, TOMOKO
 ; APPLICANT: ASHIKARI, TOSHIHIKO
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 ; FILE REFERENCE: S-38-285
 ; CURRENT APPLICATION NUMBER: US/11/217,529

```

; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166170
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-166170

```

Query Match	2.8%	Score 40;	DB 7;	Length 600;
Best Local Similarity	56.7%	Pred. No. 0.00044;		
Matches 93;	Conservative 0;	Mismatches 70;	Indels 1;	Gaps 1;
Qy	221	AGCCGAGCTCTGATTAGCTAGTCTAGTTGGTGAGGTAAGAGCTCACCAAGGCGGACGATCAGTAGC	280	
Db	428	AGCCAAATAATGGTTTTAGGTAGTAGTTTTAATAAAGTGAACCTTAGCCACGATCCCAATAAT	487	
Qy	281	GGGTCTGAGAGGATGATCCGCCACACTGGGACCTGAGACACGGCCGACACTCTCCGGGAG	340	
Db	488	CGATAATAAGTTAGAACG-ATCACGTTGACTCTGAAATATAGTCAATATCTATATGAT	546	
Qy	341	GCAGCAGTGGGGAAATTTTGGACAATGGGGGCAACCCCTGATCCAG	394	
Db	547	ACAGCAGTGGAGGAATATTGGACAATGATCAAAAGATTGATCCAG	590	

RESULT 13

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US-11-217-529-166173
; Sequence 166173, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 8-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02

```

	Query Match Best Local Similarity Matches	2.8%; 56.7%; 93;	Score 40; Pred. No. 0.00044; Conservative 0;	DB 7; Length 600; Mismatches 70;	Indels 1;	Gaps 1;
Qy	221	AGCGAGCTGATTAGCTAGTTGGTGAAGTCTACCAAGGCGAGTCAGTAGC	280			
Db	93	AGCCAAATAATGGTTTAGTGTAGTTTAAATAAAGTGAACTTAGCCACGATCCATAAT	152			
Qy	281	GGGTCTGAGAGGATGATCCGCCACACTGGGACATGAGACACGGCCGAGACTCTCTACGGGAG	340			
Db	153	CGAATAAGAAGTTAGAACG-ATCAGTGTGACTCTGAAATATAGTCNAATCTATATGAT	211			
Qy	341	GCAGCAGTGGGGAAATTTTGGACAATGGGGCAACCCCTGATCCAG	384			
Db	212	ACAGCAGTAGGAAATATTGGACAATGATCGAAAGATTGATCCAG	255			

RESULT 14

US-10-488-619-1
US-10-488-619-1
; Sequence 1, Application US/10488619

